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(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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LOCUS A48222 663 bp DNA linear PAT 07-MAR-1997

DEFINITION Sequence 1 from Patent EP0898657.

ACCESSION A48222

VERSION A48222.1 GI:2302069

KEYWORDS .

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 663)

AUTHORS De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.

TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof

JOURNAL Patent: EP 0698657-A 1 28-FEB-1996;

COMMENT SOLVAY (BE)

Other publication BE 1008751 960702

Other publication BE 1008570 960604

Other publication BR 9503454 960305

Other publication JP 8092284 960409

Other publication FI 953578 960127

Other publication CA 2154628 960127

Other publication AU 2508695 960208.

FEATURES

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Query Match 100.0%; Score 663; DB 6; Length 663;

Best Local Similarity 100.0%; Pred. No. 2,1e-169;

Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	663	100.0	663	6	A48222 Sequence 1
2	663	100.0	663	6	A48223 Sequence 2
3	663	100.0	663	6	AR193049 Sequence
4	663	100.0	663	6	AR193050 Sequence
5	663	100.0	744	6	A48225 Sequence 4
6	663	100.0	744	6	A48226 Sequence 5
7	663	100.0	744	6	AR193051 Sequence
8	663	100.0	744	6	AR193052 Sequence
9	663	100.0	1513	6	A48231 Sequence 10
10	663	100.0	1513	6	A48232 Sequence 11
11	663	100.0	1513	6	AR193055 Sequence
12	663	100.0	1513	6	AR193056 Sequence
13	634.2	95.7	744	6	A68006 Sequence 1
14	634.2	95.7	744	6	AR163110 Sequence
15	624.6	94.2	744	6	A45313 Sequence 18
16	624.6	94.2	744	6	AR117325 Sequence
17	507.8	76.6	744	6	A68016 Sequence 11
18	507.8	76.6	744	6	AR163117 Sequence
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DEFINITION	A48223		
ACCESSION	A48223		
VERSION	A48223.1	GI:2302070	
KEYWORDS	unidentified		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 663)		
AUTHORS	De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.		
TITLE	Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof		
JOURNAL	Patent: EP 0698667-A 2 28-FEB-1996;		
COMMENT	SOLVAY (BE)		
	Other publication BE 1008751 960702		
	Other publication BE 1008570 960604		
	Other publication BR 9503454 960305		
	Other publication JP 8092284 960409		
	Other publication FI 953578 960127		
	Other publication CA 2154628 960127		
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Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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DEFINITION	Sequence 1 from patent US 6346407.		
ACCESSION	AR193049		
VERSION	AR193049.1	GI:20239014	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		

Unclassified.
1 (bases 1 to 663)
De Buy, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for
preparing this xylanase and uses of the latter
Patent: US 6346407-A 1 12-FEB-2002;
JOURNAL
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Best Local Similarity 100.0%; Pred. No. 2.1e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR193050 663 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6346407.
ACCESSION AR193050
VERSION AR193050.1 GI:20239015
KEYWORDS Unknown.

ORGANISM Unknown.
Unclassified.
1 (bases 1 to 663)
De Buy, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for
preparing this xylanase and uses of the latter
Patent: US 6346407-A 2 12-FEB-2002;
JOURNAL
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Best Local Similarity 100.0%; Pred. No. 2.1e-169;
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A48225
LOCUS A48225 744 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 4 from Patent EP0698667.
ACCESSION A48225
VERSION A48225.1 GI:2302072
KEYWORDS

SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
JOURNAL Patent: EP 0698667-A 4 28-FEB-1996;
SOLVAY (BE)
COMMENT Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
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Other publication FI 953578 960127
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Best Local Similarity 100.0%; Pred. No. 2.1e-169; Mismatches 0; Indels 0; Gaps 0;
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LOCUS A48226
DEFINITION Sequence 5 from Patent EP0698667.
ACCESSION A48226
VERSION A48226.1 GI:2302073
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
JOURNAL Patent: EP 0698667-A 5 28-FEB-1996;
SOLVAY (BE)
COMMENT Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
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Other publication FI 953578 960127
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Best Local Similarity 100.0%; Pred. No. 2.1e-169; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
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LOCUS AR193051 744 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6346407.
ACCESSION AR193051
VERSION AR193051.1 GI:20239016
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
JOURNAL Patent: US 6346407-A 4 12-FEB-2002;
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ORIGIN
Query Match 100.0%; Score 663; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 2.1e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTCACGCAATTCATTTGGCAACGATGGCTATGATTAATGAAATTTGGAAA 60
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DB 202 AACAAATGTTAAACAATATTATTCGTAAGGTAAAGGTTCAATGAAGAACACAAACACAC 261
QY 181 CAACAAGTTGGTAAACATGTCATAAATACGAGGCAACTTCCAAACCAATGTAATGCG 240
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QY 241 TATTTATGCGTCTATGTTGAGCTGTGACCTCTTGTGCAATATTATATTGTCGACAGT 300
DB 322 TATTTATGCGTCTATGTTGAGCTGTGACCTCTTGTGCAATATTATATTGTCGACAGT 381
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DB 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTCGCACA 501
QY 421 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCACGATTTCTGTGAGC 480
DB 502 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCACGATTTCTGTGAGC 561
QY 481 AACCACTTTAGACGCTGGGAAACTTAGGATGAATATATGGGAAATGTATGAAGTCGCG 540
DB 562 AACCACTTTAGACGCTGGGAAACTTAGGATGAATATATGGGAAATGTATGAAGTCGCG 621
QY 541 CTTACTGTAGAGCTTCAAGTACGGAAGTCTTAATGTATATAGCAATACACTTAAGA 600
DB 622 CTTACTGTAGAGCTTCAAGTACGGAAGTCTTAATGTATATAGCAATACACTTAAGA 681
QY 601 ATTAACGGTAAACCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC 660
DB 682 ATTAACGGTAAACCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC 741
QY 661 AAT 663
DB 742 AAT 744

RESULT 8
AR193052
LOCUS AR193052 744 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5 from patent US 6346407.
ACCESSION AR193052
VERSION AR193052.1 GI:20239017
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
JOURNAL Patent: US 6346407-A 5 12-FEB-2002;
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Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 663; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 2.1e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTCACGCAATTCATTTGGCAACGATGGCTATGATTAATGAAATTTGGAAA 60
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QY 61 GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 120
DB 142 GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 201
QY 121 AACAAATGTTAAACAATATTATTCGTAAGGTAAAGGTTCAATGAAGAACACAAACACAC 180
DB 202 AACAAATGTTAAACAATATTATTCGTAAGGTAAAGGTTCAATGAAGAACACAAACACAC 261
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DB 262 CAACAAGTTGGTAAACATGTCATAAATACGAGGCAACTTCCAAACCAATGTAATGCG 321
QY 241 TATTTATGCGTCTATGTTGAGCTGTGACCTCTTGTGCAATATTATATTGTCGACAGT 300
DB 322 TATTTATGCGTCTATGTTGAGCTGTGACCTCTTGTGCAATATTATATTGTCGACAGT 381
QY 301 TGGGGCAACTGGCGTCCACGAGGAGCAACGCTTAAGGGGACCACTCACTGTTGATGGAGGA 360
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Qy      421 TTTAAACAATATGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGC 480
Db      502 TTTAAACAATATGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGC 561
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Db      562 AACCACTTTAGAGCGTGGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTGGCG 621
Qy      541 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 600
Db      622 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 681
Qy      601 ATTAACGGTAAACCTCTCTCAACTATTAGTAAATGACGAGACATAACTTTGGATAAAAC 660
Db      682 ATTAACGGTAAACCTCTCTCAACTATTAGTAAATGACGAGGATAACTTTGGATAAAAC 741
Qy      661 AAT 663
Db      742 AAT 744

RESULT 9
LOCUS   A48231 1513 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 10 from Patent EP0698667.
ACCESSION A48231
VERSION A48231.1 GI:2302078
KEYWORDS
SOURCE  unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1513)
AUTHORS De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
JOURNAL Patent: EP 0698667-A 10 28-FEB-1996;
COMMENT SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BR 1008570 960604
Other publication JP 9503454 960305
Other publication JP 8092284 960409
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508695 960208.

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ORIGIN
Query Match 100.0%; Score 663; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 2e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAAATCGTCACGACAAATTCATTGGCAACCAAGTGTATGATTAATGAATTTGGAAA 60
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Qy      61 GATAGCGGTGGCTCTCGGCAATGATTTCAATCATGCGGCGTACGTTCAAGTCCCAATGG 120
Db      761 GATAGCGGTGGCTCTCGGCAATGATTTCAATCATGCGGCGTACGTTCAAGTCCCAATGG 820
Qy      121 AACAAATGTTAACACATATATTTCCTGTAAGGTAAATTCATCAATCAACACACACAC 180
Db      821 AACAAATGTTAACACATATATTTCCTGTAAGGTAAATTCATCAATCAACACACAC 880
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Qy      181 CAAACAGTTGGTAAACATGTCATAACTACGAGCCAACTTCCAAACCAATGTAATGCG 240
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Qy      241 TATTTATGGCTCTATGTTGGACTGTTGACCTCTTGTGCGAATATATATTTGTCGACAGT 300
Db      941 TATTTATGGCTCTATGTTGGACTGTTGACCTCTTGTGCGAATATATATTTGTCGACAGT 1000
Qy      301 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGA 360
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Qy      661 AAT 663
Db      1361 AAT 1363

RESULT 10
LOCUS   A48232 1513 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 11 from Patent EP0698667.
ACCESSION A48232
VERSION A48232.1 GI:2302079
KEYWORDS
SOURCE  unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1513)
AUTHORS De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
JOURNAL Patent: EP 0698667-A 11 28-FEB-1996;
COMMENT SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BR 1008570 960604
Other publication JP 9503454 960305
Other publication JP 8092284 960409
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508695 960208.

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AUTHORS De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
TITLE Xylanase, microorganisms producing it, DNA molecules, methods for
preparing this xylanase and uses of the latter
JOURNAL Patent: US 6346407-A 11 12-FEB-2002;
FEATURES Location/Qualifiers

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ORIGIN
Query Match 100.0%; Score 663; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 2e-169;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATCGTCACCGCAATTCATTTGGCAACACGATGGCTATGATTAATGAAATTTTGAAA 60
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QY 61 GATAGCGGTGGCTCTGGGACATGATTTCTCAATCATGCGGTAGCTTCACTGCGCAATGG 120
DB 761 GATAGCGGTGGCTCTGGGACATGATTTCTCAATCATGCGGTAGCTTCACTGCGCAATGG 820
QY 121 AACATGTTTAAACATATATTTCGTAAGGTAAAAATTCATGAAACACAAACACAC 180
DB 821 AACATGTTTAAACATATATTTCGTAAGGTAAAAATTCATGAAACACAAACACAC 880
QY 181 CAACAAGTTGTPAACATGTCATATAACCTACGAGGCAACCTTCCAAACCAATGGTAATGCG 240
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QY 241 TATTTATCGCTATGTTGGACTCTGCACCTCTTGTGCAATATTATTTGTCGACAGT 300
DB 941 TATTTATCGCTATGTTGGACTCTGCACCTCTTGTGCAATATTATTTGTCGACAGT 1000
QY 301 TGGGCAACTGGCGTCCACGAGGCAACGCCCTAAAGGGGACCATCACTGTTGATGGAGGA 360
DB 1001 TGGGCAACTGGCGTCCACGAGGCAACGCCCTAAAGGGGACCATCACTGTTGATGGAGGA 1060
QY 361 ACATATGATATCTAGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTCGCCACA 420
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DB 1121 TTTTAAACAATATTGGAGTCTTCGAAGATCGAAACCGACGAGTGGCAGCATTTCTGTGAGC 1180
QY 481 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATGCGGAAAATGTATGAAGTCGCG 540
DB 1181 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATGCGGAAAATGTATGAAGTCGCG 1240
QY 541 CTTACTGTAGAAGGCTATCAAGTAGCGGAGTGTCTATGTATATAGCAATACACTAAGA 600
DB 1241 CTTACTGTAGAAGGCTATCAAGTAGCGGAGTGTCTATGTATATAGCAATACACTAAGA 1300
QY 601 ATTAACGGTAACCCCTCTCAACTATTAGTATGACGAGGATCACTTTGGATAAAAAC 660
DB 1301 ATTAACGGTAACCCCTCTCAACTATTAGTATGACGAGGATCACTTTGGATAAAAAC 1360
QY 661 AAT 663
DB 1361 AAT 1363

RESULT 13
A68006
LOCUS A68006 744 bp DNA linear PAT 05-MAY-1999
DEFINITION Sequence 1 from Patent WO9743409.
ACCESSION A68006
VERSION A68006.1 GI:4756810
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 744)
Dalboe, H., Diderichsen, B., Sandal, T. and Kauppinen, S.
METHOD OF PROVIDING NOVEL DNA SEQUENCES
JOURNAL Patent: WO 9743409-A 1 20-NOV-1997;
NOVONORDISK AS (DK)

FEATURES Location/Qualifiers
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CDS 1..744
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Query Match 95.7%; Score 634.2; DB 6; Length 744;
Best Local Similarity 97.3%; Pred. No. 1.4e-161;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 61 GATAGCGGTGGCTCTGGGACATGATTTCTCAATCATGCGGTAGCTTCACTGCGCAATGG 120
DB 142 GATAGCGGTGGCTCTGGGACATGATTTCTCAATCATGCGGTAGCTTCACTGCGCAATGG 201
QY 121 AACATGTTTAAACATATATTTCGTAAGGTAAAAATTCATGAAACACAAACACAC 180
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QY 181 CAACAAGTTGTPAACATGTCATATAACCTACGAGGCAACCTTCCAAACCAATGGTAATGCG 240
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QY 241 TATTTATCGCTATGTTGGACTCTGCACCTCTTGTGCAATATTATTTGTCGACAGT 300
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QY 301 TGGGCAACTGGCGTCCACGAGGCAACGCCCTAAAGGGGACCATCACTGTTGATGGAGGA 360
DB 382 TGGGCAACTGGCGTCCACGAGGCAACGCCCTAAAGGGGACCATCACTGTTGATGGAGGA 441
QY 361 ACATATGATATCTAGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTCGCCACA 420
DB 442 ACATATGATATCTAGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTCGCCACA 501
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DB 562 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATGCGGAAAATGTATGAAGTCGCG 621
QY 541 CTTACTGTAGAAGGCTATCAAGTAGCGGAGTGTCTATGTATATAGCAATACACTAAGA 600
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QY 601 ATTAACGGTAACCCCTCTCAACTATTAGTATGACGAGGATCACTTTGGATAAAAAC 660
DB 682 ATTAACGGTAACCCCTCTCAACTATTAGTATGACGAGGATCACTTTGGATAAAAAC 741
QY 661 AAT 663
DB 661 AAT 663

Db 742 AAT 744

RESULT 14
LOCUS AR163110 744 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6270968.
ACCESSION AR163110
VERSION AR163110.1 GI:16233600
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS Dalb.o slashed.ge,H., Sandal,T., Kauppinen,M.Sakari. and Diderichsen,Belashedge.
TITLE Method of providing a hybrid polypeptide exhibiting an activity of interest
JOURNAL Patent: US 6270968-A 1 07-AUG-2001;
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Query Match 95.7%; Score 634.2; DB 6; Length 744;
Best Local Similarity 97.3%; Pred. No. 1.4e-161; Mismatches 18; Indels 0; Gaps 0;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 CAAATCGTCACCGACAATTCATTTGGCAACACGATGGCTATGATTGATTAATTTGGAAA 60
DB 82 CAAATCGTCACCGACAATTCATTTGGCAACACGATGGCTATGATTGATTAATTTGGAAA 141
QY 61 GATAGCGGTGGCTCTGGGCAATGATCTCAATCATATGCGCGGTACGTTCAAGTCCCAATGG 120
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QY 301 TGGGGCAACTGGCGTCCACGAGCAACGCCCTAAGGGGACCACTCACTGTTGATGAGGA 360
DB 382 TGGGGCAACTGGCGTCCACGAGGCAACGCCCTAAGGGGACCACTCACTGTTGATGAGGA 441
QY 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACA 420
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QY 481 AACCACTTTAGACGCTGGGAAACTTAGGATGAATATGGGAAATGTTAAGTCCGCG 540
DB 562 AACCACTTTAGACGCTGGGAAACTTAGGATGAATATGGGAAATGTTAAGTCCGCG 621
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DB 622 CTTTACTGTAGAAGCTATCAAGTACGGAAGTGTCTAATGATATAGCAATACACTAAGA 681
QY 601 ATTTAACGGTAACCCCTCTCTCAACTATTATGTAATGACGAGAGCAATACTTTGGATATAAAC 660
DB 682 ATTTAACGGTAACCCCTCTCTCAACTATTATGTAATGACGAGAGCAATACTCTAGATATAAAC 741

QY 661 AAT 663
DB 742 AAT 744

RESULT 15
LOCUS A45313 744 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 18 from Patent WO9518219.
ACCESSION A45313
VERSION A45313.1 GI:2299796
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 744)
AUTHORS Van,S.P., Williams,D.P., Iverson,S., Farrell,R.L., Herbes,W.T., Van,D.K., Herwijer,M.A., Van,B.R., Quax,W.J., Goedegebuur,F. and Jones,B.E.
TITLE ALKALI-TOLERANT XYLANASES
JOURNAL Patent: WO 9518219-A 18 06-JUL-1995;
COMMENT GIST BROCADES NV (NL)
Other publication JP 8507221T 960806
Other publication BR 9405934 951226
Other publication NO 953312 951019
Other publication FI 953920 950821
Other publication AU 1415095 950717.
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ORIGIN

Query Match 94.2%; Score 624.6; DB 6; Length 744;
Best Local Similarity 96.4%; Pred. No. 5.8e-159; Mismatches 24; Indels 0; Gaps 0;
Matches 639; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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QY 61 GATAGCGGTGGCTCTGGGCAATGATTTCAATCATGCGGGTACGTTCAAGTCCCAATGG 120
DB 139 GATAGCGGTGGCTCTGGGCAATGATTTCAATCATGCGGGTACGTTCAAGTCCCAATGG 198
QY 121 AACATGTTAAACAACATATTTCCGTAAGGTAAAGATTTCAATGAAACACACACAC 180
DB 199 AATAATGTTAAACAATATATTTCCGTAAGGTAAAGATTTCAATGAAACACACACAC 258
QY 181 CAACAAGTTGGTAACATGTCATATACTAGGAGCAACTTCCAAACCAATGTTAATGCG 240
DB 259 CAACAAGTTGGTAACATGTCATATACTAGGAGCAACTTCCAAACCAATGTTAATGCG 318
QY 241 TATTTATGCGTCTATGTTGAGCTGTGACCCCTCTTGTGCAATATTAATTTGCGACAGT 300
DB 319 TATTTATGCGTCTATGTTGAGCTGTGACCCCTCTTGTGCAATATTAATTTGCGACAGT 378
QY 301 TGGGGCAACTGGCGTCCACGAGGACCAACCCCTAAGGGGACCACTCTGTTGATGAGGA 360
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Qy	361	ACATATGATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGATTGCCACA	420
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Qy	421	TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGC	480
Db	499	TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGC	558
Qy	481	AACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATGGGAAATGTATGAAAGTCGCG	540
Db	559	AACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATGGGAAATGTATGAAAGTCGCG	618
Qy	541	CTTACTGTAGAAGGCTATCAAGTAGCGGAAGTCTAATGTATATAGCAATACACTAAGA	600
Db	619	CTTACTGTAGAAGGCTATCAAGTAGCGGAAGTCTAATGTATATAGCAATACACTAAGA	678
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Qy	661	AAT 663	
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Perfect score: 185
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Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_est9:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	37.6	20.3	1281	9	AG346331 Mus muscu
2	37.4	20.2	865	9	AG388392 Mus muscu
3	37.2	20.1	628	1	AL867917 AL867917
4	37.2	20.1	659	1	AL846715 AL846715
5	37.2	20.1	663	5	BQ527682 NISC.no23
6	37.2	20.1	880	7	CR584662 CR584662
C 7	37.2	20.1	955	5	EX772034 BX772034
8	36	19.5	909	8	AZ549992 ENTGS63TF
C 9	35.8	19.4	714	9	CE215054 tigr-gss-
C 10	35.8	19.4	1101	9	CNS017L2 Drosophil
C 11	35.6	19.2	352	7	CR449406 CR449406
C 12	35.6	19.2	833	8	BZ224970 CH230-351
C 13	35.6	19.2	874	7	CR579359 CR579359
C 14	35.6	19.2	960	1	AL901596 AL901596
C 15	35.4	19.1	951	4	BG164591 602342154
C 16	35.2	19.0	732	9	AG343254 Mus muscu
C 17	35	18.9	444	7	CN450127 GUO cdna
C 18	35	18.9	686	7	CN450126 GUO cdna
C 19	35	18.9	911	8	CC386284 PUHTN23TB
C 20	34.8	18.8	500	8	AQ154047 HS_2236_B
C 21	34.6	18.7	485	2	BF702386 MI-P-H3-a
C 22	34.6	18.7	523	4	BJ644137 BJ644137
C 23	34.6	18.7	703	4	BJ641803 BJ641803
C 24	34.6	18.7	867	4	BG539277 602567876

C 25	34.6	18.7	921	9	CL264923
C 26	34.4	18.6	203	8	AZ037080
C 27	34.2	18.5	529	7	CN055278
C 28	34	18.4	492	9	CE103446
C 29	34	18.4	593	2	AW645414
C 30	34	18.4	636	9	DR28A11S
C 31	34	18.4	796	9	CL283976
C 32	34	18.4	1029	5	BX424910
C 33	33.8	18.3	619	5	BW308307
C 34	33.8	18.3	679	6	CF180381
C 35	33.8	18.3	681	9	CL551099
C 36	33.8	18.3	697	8	BH965893
C 37	33.8	18.3	721	8	BH965366
C 38	33.8	18.3	724	9	CL509951
C 39	33.8	18.3	737	5	BW183846
C 40	33.6	18.2	536	9	CE133665
C 41	33.6	18.2	570	8	AZ908959
C 42	33.6	18.2	609	9	CE263180
C 43	33.6	18.2	621	9	CE202395
C 44	33.6	18.2	700	8	AZ909070
C 45	33.6	18.2	733	9	AG380466

ALIGNMENTS

RESULT 1
AG346331/c
LOCUS
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-141H11.T7, genomic survey
sequence.
ACCESSION AG346331 GI:47919641
VERSION AG346331.1
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1281)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, URL: http://hgp.gsc.riken.go.jp/
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center, Research (RIKEN) 3-1-1
Koyada, Tsukuba, 305-0074 Japan
Phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBAC3.6
R.Site 1 : EORI
R.Site 2 : EORI
FEATURES
Location/Qualifiers
1. : 1281
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-141H11.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

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ORIGIN
Query Match      20.3%; Score 37.6; DB 9; Length 1281;
Best Local Similarity 52.7%; Pred. No. 2.1;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 36 AAAGGATTATACACAAACAGAGACATCCATGCGGGTTAAAGCAGTATCGTTCCATCT 95
DB 1225 AAAGAAGGTGAAGATCAAGAGAAAATAACCATGCAAAAGTAAGAGATAAATCTTTTATAA 1166
QY 96 AACAGAGAAGNCTGCATCAAGAGAGGTGATGGGTTTTCATCTTAGGGATGACAGAA 155
DB 1165 AAGATAGATAAATAAAGGAATAGAGTATAATGNTATTGAAGTTGAGAGACAAAAA 1106
QY 156 ATACGGATCAAAAGAGAGAGGTGGA 185
DB 1105 ATAGGATGAGAGAGAGAAATGATGAA 1076

RESULT 2
AG388392
LOCUS Mus musculus molossinus DNA, clone:MSMg01-203L20.TJ, genomic survey
DEFINITION
ACCESSION AG388392.1 GI:47999597
VERSION AG388392.1
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
REFERENCE 1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
AUTHORS BAC end Sequences of Library MSMg01
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 865)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY : pBACe3.6
Vector :
R.Site 1 : EcoRI
R.Site 2 : EcoRI
FEATURES
source
Location/Qualifiers
1..865
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-203L20.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match      20.2%; Score 37.4; DB 9; Length 865;
Best Local Similarity 50.3%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 21 TATTTTCATTTGTATCAAAAGGATTTTATACAAACAGAGACATCCATGCGGGTTAAAGC 80
DB 1225 AAAGAAGGTGAAGATCAAGAGAAAATAACCATGCAAAAGTAAGAGATAAATCTTTTATAA 1166
QY 96 AACAGAGAAGNCTGCATCAAGAGAGGTGATGGGTTTTCATCTTAGGGATGACAGAA 155
DB 1165 AAGATAGATAAATAAAGGAATAGAGTATAATGNTATTGAAGTTGAGAGACAAAAA 1106
QY 156 ATACGGATCAAAAGAGAGAGGTGGA 185
DB 1105 ATAGGATGAGAGAGAGAAATGATGAA 1076

RESULT 3
AL867917
LOCUS AL867917 XGC-egg Xenopus tropicalis cDNA clone TEGg105m20 5', mRNA
DEFINITION
ACCESSION AL867917
VERSION AL867917.2 GI:38663115
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
REFERENCE 1 (bases 1 to 628)
AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT On Sep 15, 2002 this sequence version replaced gi:22888182.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
TROPICALIS_SEQUENCE_ID: TEGg105m20.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site1: EcoRI; Site 2: NotI
Host: Escherichia coli Xli-blue.
FEATURES
source
Location/Qualifiers
1..628
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEGg105m20"
/dev_stage="egg"
/lab_host="Escherichia coli Xli-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      20.1%; Score 37.2; DB 1; Length 628;
Best Local Similarity 58.9%; Pred. No. 2.4;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 16 TGATCTATTTTCATTTGTATCAAGATTTATACAAACAGAGACATCCATGCGGGTT 75
DB 500 TGCTACTAGATAAAATATCCCAAGAAATTTATAAGAACAAAGACATTTATGAGGAAT 559
QY 76 AAAGCAGTATCGTTCCATCTAACAGAGAGCGNCTGCATGCAAGAGG 122
DB 560 GAAGGAGTATGCGCCCTGCTACACTTTTGTGCTGTCATCTCGAGGAAG 606

RESULT 4

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AL846715	AL846715	XGC-egg	Xenopus tropicalis	cDNA clone	TEGG049119	5'	mRNA	linear	EST 20-NOV-2003
LOCUS	AL846715	sequence.							
DEFINITION	AL846715	sequence.							
ACCESSION	AL846715	GI:38487703							
VERSION	AL846715								
KEYWORDS	EST.								
SOURCE	Xenopus tropicalis	(western clawed frog)							
ORGANISM	Xenopus tropicalis								
	Eukaryota;	Metazoa;	Chordata;	Craniata;	Vertebrata;	Euteleostomi;			
	Amphibia;	Batrachia;	Anura;	Mesobatrachia;	Pipoidae;				
	Xenopodinae;	Xenopus;	Silurana.						
REFERENCE	1 (bases 1 to 659)								
AUTHORS	Croning,M.D.R.,	Ashurst,J.L.,	Taylor,R.,	Zorn,A.M.	and	Rogers,J.			
TITLE	Sanger Xenopus tropicalis	EST project	2001	(11_2003)					
JOURNAL	Unpublished	(2003)							
COMMENT	On Sep 15, 2002 this	sequence	version	replaced	gi:	228665980.			

Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: Tegg049i19.plksp6w
Sequencing primer: Sp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5', end and NotI at the 3', end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: *Escherichia coli* XL1-blue.

FEATURES
source

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1. .659
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:3364"
/clone="T99049119"
/lab_host="egg"
/lab_host="Escherichia coli XL1"
/clone_lib="XCG-egg"
/notes="Vector: pCS107; Site 1: was oligo dT primed from sug
ECORI-NotI cut cDNA was then l
ECORI at the 5' end and NotI a

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ORIGIN

Position	Sequence	Score	DB 1	Length	659
16	TCATCTATTTCATTTGGTATCAAAGGATTTATACACAAACAAGACACATCCATATGCCGGGTT	20.1%;	DB 1	Length 659	
421	TGTACTAGTAAAAATATCCCAAAGAATTTATAAAGAACAAAGACTTATTATGAGGAATT	58.9%;	Pred. No. 2,5;		
76	AAAGCAGTATCGTTCATCTACACAGAAGNCTGCATGAAGAGG	63;	Conservative	0; Mismatches	44; Indels
481	GAAGCAGTATGACCTCTCTACATCTTGTGTTCTCATCTCAGGAAG	0;			

BQ527682 663 bp . mRNA linear EST 10-JUN-2002
NISC no23g06.y1 NICHD_XC_Emb8 *Xenopus tropicalis* cDNA clone
IMAGE:5381962 5' . mRNA sequence.

RQ527682
 RQ527682.1 GI:21386551
 EST.
 Xenopus tropicalis (western clawed frog)
 Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 663)

AUTHORS	JOURNAL
TITLE	COMMENT
W. J. G. B. van den Broek J. H. M. A. van der Vlist J. H. M. A. van der Vlist J. H. M. A. van der Vlist	

NIH-XCG <http://image.llnl.gov/image/html/xenopuslib.info.shtml>.
National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
Unpublished (2002)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
[info/image.llnl.gov](http://image.llnl.gov/info/image.llnl.gov)
Plate: LLAM11972 row: N column: 11
Seq primer: M13Rp1 reverse primer (ABI).

FEATURES
SOURCE

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1. .663
   /organism="Xenopus tropicalis"
   /mol_type="mRNA"
   /db_xref="taxon:8364"
   /clone="IMAGE:5381962"
   /tissue_type="tadpole"
   /dev_stage="embryo, stages 40-
   /lab_host="PHIOB (phage-resistant
   /clone_lib="NICHG XGC Embs"
   /notes="Vector: pCMV-SPORT6.1;
   /cloned_unidirectionally: 1 primer
   size 2.1 kb. Constructed by In
   xenopus Gene Collection (XGC)

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ORIGIN

Match	20.1%;	Score 37.2;	DB 5;	Length 663;
Local Similarity	58.9%;	Pred No. 2.5;		
63; Conservative	0;	Mismatches	44;	Indels 0; Gaps 0;

16	TGATCATTTTCATTGTTATCAAAAGGATTTATACAAACAGAGACATCCATGCCGGTT	75
345	TGTACTAGATAAAATATCCCAAGAATTTATTAAGAAACAAGAAGCTATTATGAGGAATT	404
76	AAAGCAGTATCGTTCCATCTAACAGAGAGGNCCTCATCGAAGGAGG	122
405	GAAGGAGTATGGCCCTGTCTACACTTTGTGGTCTGCATCTGAGGAAG	451

RESIN.T 6

CR584662 880 bp mRNA linear EST 26-JUL-2004
CR584662 XGC-tailbud-head Xenopus tropicalis cDNA clone THd043p12
5', mRNA sequence.
CR584662
CR584662.1 GI:50584662
EST.
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 880)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (2004)
Unpublished (2004)
Contact: Croning MDR

FEATURES

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1. .880
/organism="Xenopus tropicalis"
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/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="THA042p12"
/dev_stage="tailbud head (stage 28-30)"
/lab_host="Escherichia coli DH10B."
/clone_lib="XGC-tailbud-head"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from Sug of poly A+ RNA from tailbud head. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
Query Match 20.1%; Score 37.2; DB 7; Length 880;
Best Local Similarity 58.9%; Pred. No. 2.6;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 16 TGATCTATTTCATTGTTCAAGGATTTATACACAAAGAGACATCCATGCCGGTT 75
DDB 641 TTCTACTAGTAATAATATCCCAAGATTTATAGACAAAGACTATTATGAGGAAT 700

QY 76 AAAGCAGTATCGTTCCTCTAACAGAGAAGNCTGCATGAAAGGAGG 122
DDB 701 GAAGGAGTATGSCCTGTCTACACTTGTGCTGCTGATCGAGGAAG 747

RESULT 7
BX772034/c
LOCUS BX772034 XGC-egg Xenopus tropicalis cDNA clone TEGG049g14 3', mRNA
DEFINITION
ACCESSION BX772034
VERSION BX772034.1 GI:39679239
KEYWORDS
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
UNPUBLISHED (2003)
CONTACT: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEGG049g14.q1k77
Sequencing primer: 77
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1. .955
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEGG049g14"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match 20.1%; Score 37.2; DB 5; Length 955;
Best Local Similarity 58.9%; Pred. No. 2.6;

/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="THA042p12"
/dev_stage="tailbud head (stage 28-30)"
/lab_host="Escherichia coli DH10B."
/clone_lib="XGC-tailbud-head"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from Sug of poly A+ RNA from tailbud head. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
Query Match 19.5%; Score 36; DB 8; Length 909;
Best Local Similarity 50.3%; Pred. No. 6;
Matches 87; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 11 GCGCTTGATCTATTTCATTGTTCAAGGATTTATACAAAGAGCATCCATGCC 70
DDB 583 CACCAGGATATGTTGGATATGAAGAGGAGGACATTAAACAGAGCAATTCGTGTAGAC 642

QY 71 GGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGNCTGCATGAAAGGAGGTGATGGGT 130
DDB 643 CATATAGTGTATATATTATTTGATGNAATTGAAGAGCACATCCACAAAGTATTAATGTTGT 702

Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 16 TGATCTATTTCATTGTTCAAGGATTTATACACAAAGAGACATCCATGCCGGTT 75
DDB 944 TGTACTAGTATAAATATCCCAAGATTTATAGACAAAGACTATTATGAGGAAT 885

QY 76 AAAGCAGTATCGTTCCTCTAACAGAGAAGNCTGCATGAAAGGAGG 122
DDB 884 GAAGGAGTATGSCCTGTCTACACTTGTGCTGCTGATCGAGGAAG 838

RESULT 8
AZ549992
LOCUS AZ549992
DEFINITION AZ549992 Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000
genomic, genomic survey sequence.
ACCESSION AZ549992
VERSION AZ549992.1 GI:11175146
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 909)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
UNPUBLISHED (2000)
CONTACT: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 22
High quality sequence stop: 762.
FEATURES
source
1. .909
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOSI; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

ORIGIN
Query Match 19.5%; Score 36; DB 8; Length 909;
Best Local Similarity 50.3%; Pred. No. 6;
Matches 87; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 11 GCGCTTGATCTATTTCATTGTTCAAGGATTTATACAAAGAGCATCCATGCC 70
DDB 583 CACCAGGATATGTTGGATATGAAGAGGAGGACATTAAACAGAGCAATTCGTGTAGAC 642

QY 71 GGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGNCTGCATGAAAGGAGGTGATGGGT 130
DDB 643 CATATAGTGTATATATTATTTGATGNAATTGAAGAGCACATCCACAAAGTATTAATGTTGT 702

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[illegible]

[illegible]

LOCUS AL901596 960 bp mRNA linear EST 04-DEC-2003
DEFINITION AL901596 XGC-egg Xenopus tropicalis cDNA clone TEGG021j23 3', mRNA
sequence.
ACCESSION AL901596
VERSION AL901596.2 GI:38700171
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 960)
AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Sanger Xenopus tropicalis EST project 2001 (11_2003)
COMMENT On Sep 16, 2002 this sequence version replaced gi:22953805.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEGG021j23.q1kT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
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EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
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Best Local Similarity 57.9%; Pred. No. 8;
Matches 62; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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RESULT 15
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LOCUS BG164591 951 bp mRNA linear EST 06-FEB-2001
DEFINITION 602342154F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4452252 5',
mRNA sequence.
ACCESSION BG164591
VERSION BG164591.1 GI:12671294
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 951)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIAW10240 row: 1 column: 13
High quality sequence stop: 717.
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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Best Local Similarity 53.7%; Pred. No. 9.2;
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QY 92 ATCTAACAGAGAGGNCCTGCATGAAGAGGAGTGATGGGTTTTTCATCTTAGGGATGACAG 151
Db 491 GCGCCACATAGAGAATGAATGAAGAAAGCTTTAGAAAAGCTTGATGTGAAGCAAAACAG 550
QY 152 AACAAATACGGATGA 165
Db 551 AACTAGAATCATTA 564

Search completed: November 11, 2004, 01:16:56
Job time : 805.957 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 10, 2004, 15:57:32 ; Search time 391.831 Seconds
(without alignments)
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Perfect score: 81
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 12: gb_sv.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	81	100.0	81	6	A42283 Sequence 33
3	81	100.0	81	6	A48248 Sequence 27
4	81	100.0	81	6	A48249 Sequence 28
5	81	100.0	81	6	AR127042 Sequence
6	81	100.0	81	6	AR127047 Sequence
7	81	100.0	81	6	AR193072 Sequence
8	81	100.0	81	6	AR193073 Sequence
9	81	100.0	81	6	AR220046 Sequence
10	81	100.0	81	6	AR220051 Sequence
11	81	100.0	81	6	AR221329 Sequence
12	81	100.0	81	6	AR221334 Sequence
13	81	100.0	681	6	A42280 Sequence 30
14	81	100.0	681	6	A42282 Sequence 32
15	81	100.0	681	6	AR127045 Sequence
16	81	100.0	681	6	AR127046 Sequence
17	81	100.0	681	6	AR220049 Sequence
18	81	100.0	681	6	AR220050 Sequence
19	81	100.0	681	6	AR221332 Sequence

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27	81	100.0	1022	6	AR221306
28	81	100.0	1022	6	AR221336
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ALIGNMENTS

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DEFINITION Sequence 27 from Patent EP0634490.
ACCESSION A42277
VERSION A42277.1 GI:2297765
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 81)
AUTHORS De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.
TITLE Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
JOURNAL Patent: EP 0634490-A 27 18-JAN-1995;
COMMENT SOLVAY (BE)
Other publication NZ 260989 950828
Other publication BR 9402834 950613
Other publication JP 7067637 950314
Other publication FI 943389 950116
Other publication CA 2128050 950116
Other publication AU 6743294 950127
Other publication GB 2279955 950118.

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Db 1 ATGAATTGAAAGATTGAGCGTGTGTGTGATGTATTGGATTGTGCTGACACTG 60
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ORGANISM	Bacillus pumilus	
REFERENCE	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
AUTHORS	1 (bases 1 to 81)	
TITLE	De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.	
JOURNAL	Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof	
COMMENT	Patent: EP 0634490-A 33 18-JAN-1995; SOLVAY (BE)	
OTHER PUBLICATION	NZ 260989 950828	
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SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 81)									
AUTHORS	De Buyl,E., Lahaye,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.									
TITLE	Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof									
JOURNAL	Patent: US 6180382-A 27 30-JAN-2001;									
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ACCESSION	AR127047									
VERSION	AR127047.1 GI:14113640									
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SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 81)									
AUTHORS	De Buyl,E., Lahaye,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.									
TITLE	Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof									
JOURNAL	Patent: US 6180382-A 33 30-JAN-2001;									
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DEFINITION	Sequence 27 from patent US 6346407.									

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	DEFINITION	Sequence 30 from Patent EP0634490.				
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	REFERENCE	1 (bases 1 to 681)				

AUTHORS	De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.
TITLE	Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
JOURNAL	Patent: EP 0634490-A 30 18-JAN-1995;
COMMENT	SOLVAY (BE) Other publication NZ 260989 950828 Other publication BR 9402834 950613 Other publication JP 7067637 950314 Other publication FI 943389 950116 Other publication CA 2128050 950116 Other publication NO 942852 950116 Other publication AU 6743294 950127 Other publication GB 2279955 950118.
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DEFINITION	Sequence 32 from Patent EP0634490.
ACCESSION	A42282
VERSION	A42282.1 GI:2297769
KEYWORDS	
SOURCE	Bacillus pumilus Bacillus pumilus Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE	1 (bases 1 to 681)
AUTHORS	De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.
TITLE	Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
JOURNAL	Patent: EP 0634490-A 32 18-JAN-1995;
COMMENT	SOLVAY (BE) Other publication NZ 260989 950828 Other publication BR 9402834 950613 Other publication JP 7067637 950314 Other publication FI 943389 950116 Other publication CA 2128050 950116 Other publication NO 942852 950116 Other publication AU 6743294 950127 Other publication GB 2279955 950118.
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 15:55:17 ; Search time 51.3814 Seconds
(without alignment)
8275.436 Million cell updates/sec

Title: US-09-909-207-27
Perfect score: 81
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues 8269772
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	29.4	36.3	508	10	AdE81488 Arabidops
7	29.4	36.3	1138	3	AaC52006 Arabidops
8	29.4	36.3	1216	3	AaC37584 Arabidops
9	28.6	35.3	1183	5	AbV29555 Human pro
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11	28.4	35.1	1380	6	AbN66065 Streptoco
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17	27.4	33.8	2790	1	AaN60473 Sequence
18	27.4	33.8	4106	10	AdD45341 Rat gene
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	30	26.6	32.8	13033	4	ABL14054	Abi14054 Drosophil
	31	26.4	32.6	3234	12	ADP09637	Adp09637 Rice heat
	32	26.2	32.3	727	6	ABs77245	ABs77245 Frog heat
	33	26.2	32.3	1959	11	ADL72389	AdL72389 Cascor lo
	34	26.2	32.3	3915	4	ABL04067	AbL04067 Drosophil
	35	26.2	32.3	6147	3	AAZ53858	AaZ53858 Neisseria
	36	26.2	32.3	6197	4	ABL04066	AbL04066 Drosophil
	37	26.2	32.3	39746	4	ABL13398	Abi13398 Drosophil
	38	26.2	32.3	110000	3	AAZ22303_1	Continuation (2 of
	39	26.2	32.3	110000	6	ABR90521_08	Continuation (9 of
	40	26	32.1	9741	6	ABL33323	Ade60106 Rat gene
	41	26	32.1	11049	6	ABL33323	Abi33323 Human imm
	42	26	32.1	11049	6	ABL32668	Abi32668 Human imm
	43	26	32.1	11049	6	ABL92218	Abi92218 Chemical
	44	26	32.1	11049	6	ABL49321	Abi49321 Human pol
	45	26	32.1	114693	8	AA48308	Aa48308 Human tra

ALIGNMENTS

RESULT 1
AAQ73997
ID AAQ73997 standard; DNA; 81 BP.
XX
AC AAQ73997;
XX
DT 16-OCT-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
DE Xylanase gene presequence.
XX
XX Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
KW promoter; signal peptide; ss.
XX
OS Bacillus pumilus; strain PRL B12 (ATCC 55443).
XX
PN AU9525086-A.
XX
PD 08-FEB-1996.
XX
PF 19-JUL-1995; 95AU-00025086.
XX
PR 26-JUL-1994; 94BE-00000706.
PR 17-MAY-1995; 95BE-00000448.
XX
(SOLV) SOLVAY SA.
XX
PI De Buyl E, Lahaye A, Ledoux P, Detroz R;
XX
XX WPI; 1996-117341/13.
DR P-PSDB; AAR92055.
XX
PT Bacillus derived xylanase active over wide pH range - used in treatment
of paper pulp, animal feeds and in bakery goods.
XX
XX Claim 27; Page 70; 94pp; English.
XX
CC The Bacillus pumilus PRL B12 xylanase gene presequence (AAQ73997)
encoding the xylanase signal peptide (AAR92055) was incorporated along
with the promoter sequence (AAQ73996) into vectors used for the
expression of DNA (see AAT16101) coding for a mature, thermostable
xylanase (AAR92053) of Bacillus sp. 720/1. The enzyme is produced in
transformed hosts, pref. Bacillus licheniformis or B. pumilus, for use in
the paper pulp, animal feed and baking industries. (Updated on 16-OCT-

[illegible]

XX Arabidopsis thaliana expressed polynucleotide seq id 259.
DE
XX genetically modified organism; transgenic organism; plant;
KW inhibitor testing; activator testing; modifier testing; fungicide;
KW insecticide; genetic function; genetic regulation; cellular metabolism;
KW gene; ss.
XX
XX Arabidopsis thaliana.
XX
XX US2003115639-A1.
XX
XX 19-JUN-2003.
XX
XX 26-JAN-2001; 2001US-00770961.
XX
XX 27-JAN-2000; 2000US-0178466P.
XX
XX (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX
XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
XX WPI; 2003-810930/76.
XX
XX Novel Arabidopsis thaliana nucleic acids useful for generating
PT genetically modified transgenic organisms, for screening biologically
PT active agents such as fungicides, insecticides.
XX
XX Claim 1; SEQ ID NO 259; 44pp; English.
XX
XX The invention describes a nucleic acid (1) comprising a sequence capable
CC of hybridising under stringent conditions to any one of 999 fully defined
CC Arabidopsis thaliana sequences (1) as given in specification e.g., 360,
CC 1137, 455, 219, 472 nucleotides, etc, or its fragment. (1) is useful as a
CC hybridisation probe to complementary molecules in a cDNA library. (1) is
CC also useful for generating genetically modified and transgenic organisms,
CC usually plant cells and plants. A protein encoded by (1) is useful in
CC screening assays to determine the effect of candidate inhibitors,
CC activators or modifiers of the gene product. The protein is also useful
CC for screening biologically active agents e.g., fungicides and
CC insecticides. A genetically modified cell, comprising an exogenous
CC nucleic acid, where the nucleic acid comprises transcription regulatory
CC sequences operably linked to a sequence capable of hybridising under
CC stringent conditions to (1) is useful in the study of genetic function
CC and regulation, for alteration of the cellular metabolism and for
CC screening compounds that may affect the biological function of the gene
CC or gene product. This sequence represents an Arabidopsis thaliana
CC polynucleotide of the invention.
XX
XX Sequence 508 BP; 165 A; 109 C; 90 G; 144 T; 0 U; 0 Other;
SQ

Query Match

36.3%; Score 29.4; DB 10; Length 508;

Best Local Similarity 70.9%; Pred. No. 6.9;
Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Oy 1 ATGATTTGAAAGATTGAGCTGTTGTTTGTGATGTGATTTGCTGA 55
Db 159 ATGCATGTGAAAGCTTTGATGATGATGCTTTTGTGTTGCTGCTGCTGA 105

RESULT 7

AAC52006
ID AAC52006 standard; DNA; 1138 BP.

XX AAC52006;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 70190.

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 28-APR-1999; 99US-0130891P.

XX 30-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132407P.

XX 04-MAY-1999; 99US-0132484P.

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XX 06-MAY-1999; 99US-0132486P.

XX 06-MAY-1999; 99US-0132487P.

XX 07-MAY-1999; 99US-0132863P.

XX 11-MAY-1999; 99US-0134256P.

XX 14-MAY-1999; 99US-0134218P.

XX 14-MAY-1999; 99US-0134219P.

XX 14-MAY-1999; 99US-0134221P.

XX 18-MAY-1999; 99US-0134370P.

XX 18-MAY-1999; 99US-0134768P.

XX 19-MAY-1999; 99US-0134941P.

XX 20-MAY-1999; 99US-0135124P.

XX 21-MAY-1999; 99US-0135353P.

XX 24-MAY-1999; 99US-0135629P.

XX 25-MAY-1999; 99US-0136021P.

XX 27-MAY-1999; 99US-0136392P.

XX 28-MAY-1999; 99US-0136782P.

XX 01-JUN-1999; 99US-0137222P.

XX 03-JUN-1999; 99US-0137528P.

XX 04-JUN-1999; 99US-0137502P.

XX 07-JUN-1999; 99US-0137724P.

XX 08-JUN-1999; 99US-0138094P.

XX 10-JUN-1999; 99US-0138540P.

XX 10-JUN-1999; 99US-0138847P.

XX 14-JUN-1999; 99US-0139119P.

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ID AAC37584 standard; DNA; 1216 BP.
XX
AC AAC37584;
XX
DT 17-OCT-2000 (first entry)
XX
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17922.
XX
XX Hybridisation assay; Genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX
PD 06-SEP-2000.
XX
PF
XX 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
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PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.

XX	RESULT 9	XX	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
ABV29555/c		KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
ID	ABV29555 standard; cDNA; 1183 BP.	KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX		XX	pharmacogenomic marker; gene; ss.
AC	ABV29555;	OS	Homo sapiens.
yy		XX	Homo sapiens.


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Query Match      34.6%; Score 28; DB 10; Length 110000;
Best Local Similarity 63.2%; Pred. No. 91;
Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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9 GAAAAGATTGAGCGCTGTTTGTGTCATGTCATTTCGATTTTGTCTGCACACTGACCGCGTGT 68

RESULT 15
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ID AAI93584 standard; cDNA; 3623 BP.
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XX AAI93584;
AC
XX
DT
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 13644.
XX

XX
PF 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
PR
XX (HYSE-) HYSEQ INC.
PA

Tang YT, Liu C, Drmanac RT;
PI
XX
DR WPI; 2001-514838/56.
DR P-PSDB; AA013653.

Claim 1; SEQ ID NO 13644; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation of which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoietic regulatory activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at wipo.int/pub/publ/published/pct/sequences

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X      Query Match      34.3%;      Score 27.8;      DB 4;      Length 3623;
K      Best Local Similarity 65.1%;      Pred. No. 41;
      Matches 41;      Conservative 0;      Mismatches 22;      Indels 0;      Gaps 0
Q      Sequence 3623 BP; 1143 A; 501 C; 572 G; 1303 T; 0 U; 104 Other;

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Qy

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Qy

6 TTTGAAAAGATTGAGCGCTGTGTTTTGTCATGTCGTATTGGATTTTGTGCTGCACACTGACCGC 65

Db 2724 TTGATATAGATATATGATATTGATTCTCGAGCTGCTTTTGTATTTTCTGACTTTGGCATC 2783

Qy 66 TGT 68

Db 2784 TGT 2786

Search completed: November 10, 2004, 17:09:40
Job time : 54.3814 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 17:09:58 ; Search time 9.30509 Seconds
(without alignments)
6187.359 Million cell updates/sec

Title: US-09-909-207-27
Perfect score: 81
Sequence: 1 ATGATTTTGAAGAATTGAG.....CGCTGTGCGGCTCATGG 81

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	81	3	US-08-275-526C-27
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5	81	100.0	81	4	US-09-076-677-27
6	81	100.0	81	4	US-09-076-677-33
7	81	100.0	81	4	US-09-073-055-27
8	81	100.0	81	4	US-09-073-055-33
9	81	100.0	681	3	US-08-275-526C-30
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24	26.2	32.3	324	4	US-09-614-221A-198
25	26.2	32.3	726	4	US-09-248-796A-9223
26	26	32.1	11049	4	US-10-204-708-21
27	25.4	31.4	262	4	US-09-313-294A-1889

c	28	25.4	31.4	1317	4	US-09-248-796A-5112	Sequence 5112, Ap
c	29	25.2	31.1	1710	3	US-09-068-960-14	Sequence 14, Appl
c	30	25	30.9	564	4	US-09-248-796A-596	Sequence 596, App
c	31	25	30.9	1377	4	US-09-134-000C-3078	Sequence 3078, Ap
c	32	25	30.9	2013	4	US-09-543-681A-1807	Sequence 1807, Ap
c	33	25	30.9	4487	4	US-09-484-970B-96	Sequence 96, Appl
c	34	25	30.9	36412	4	US-08-311-731A-132	Sequence 132, App
c	35	24.8	30.6	849	4	US-09-248-796A-7183	Sequence 7183, Ap
c	36	24.8	30.6	1230	4	US-09-248-796A-1393	Sequence 1393, Ap
c	37	24.8	30.6	1963	5	PCT-US91-07715A-1	Sequence 1, Appl
c	38	24.8	30.6	1970	1	US-07-596-867C-1	Sequence 1, Appl
c	39	24.8	30.6	1664976	4	US-08-916-421B-1	Sequence 1, Appl
c	40	24.8	30.6	1664976	4	US-09-692-570-1	Sequence 1, Appl
c	41	24.6	30.4	1513	4	US-09-301-666A-9	Sequence 9, Appl
c	42	24.6	30.4	1513	4	US-09-301-217-9	Sequence 9, Appl
c	43	24.6	30.4	2106	4	US-09-248-796A-2525	Sequence 2525, Ap
c	44	24.4	30.1	1236	4	US-09-248-796A-6578	Sequence 6578, Ap
c	45	24.4	30.1	2542	3	US-08-941-445A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
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; Sequence 27, Application US/08275526C
; Patent No. 6180382
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: LAHAYE, ANDR E
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE
; APPLICANT: DETROZ, REN
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-275-526C-27

Query Match 100.0%; Score 81; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTGAAAGATTGAGGCTGTTGTTGATGATGATTTGGATTGCTGACACTG 60
DB 1 ATGAATTTGAAAGATTGAGGCTGTTGTTGATGATGATTTGGATTGCTGACACTG 60

QY 61 ACGGCTGTGCCGCTCATGCG 81
DB 61 ACGGCTGTGCCGCTCATGCG 81

RESULT 2

US-08-275-526C-33

; Sequence 33, Application US/08275526C

; Patent No. 6180382

; GENERAL INFORMATION:

; APPLICANT: DE BUYL, ERIC

; APPLICANT: LAHAYE, ANDR E

; APPLICANT: LEDOUX, PIERRE

; APPLICANT: AMORY, ANTOINE

; APPLICANT: DETROZ, REN

; APPLICANT: ANDRE, CHRISTOPHE

; APPLICANT: VETTER, ROMAN

; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,

; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND

; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND

; TITLE OF INVENTION: USE THEREOF

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.

; STREET: 2000 K St., N.W., Suite 200

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/275,526C

; FILING DATE: 15-JUL-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Gadiano, Wilhem F.

; REGISTRATION NUMBER: 37,136

; REFERENCE/DOCKET NUMBER: 4121-49

; TELEPHONE: (202) 429-0625

; TELEFAX: (202) 293-0625

; TELEX: 650 383 5605

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 81 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; ORIGINAL SOURCE: Bacillus pumilus

; ORGANISM: Bacillus pumilus

; STRAIN: PRL B12

; US-08-275-526C-33

; Query Match 100.0%; Score 81; DB 3; Length 81;

; Best Local Similarity 100.0%; Pred. No. 1.8e-19;

; Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 ATGAATTTGAAAGATTGAGGCTGTTGTTGATGATGATTTGGATTGCTGACACTG 60

; DB 1 ATGAATTTGAAAGATTGAGGCTGTTGTTGATGATGATTTGGATTGCTGACACTG 60

QY 61 ACGGCTGTGCCGCTCATGCG 81
DB 61 ACGGCTGTGCCGCTCATGCG 81

RESULT 3

US-08-470-953A-27

; Sequence 27, Application US/08470953A

; Patent No. 6346407

; GENERAL INFORMATION:

; APPLICANT: ANDREE LAHAYE

; APPLICANT: ERIC DE BUYL

; APPLICANT: PIERRE LEDOUX

; APPLICANT: RENE DETROZ

; TITLE OF INVENTION: Xylanase, microorganisms produced it,

; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

; TITLE OF INVENTION: and uses thereof

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE

; STREET: 2000 K St., N.W., Suite 200

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,953A

; FILING DATE: 6-OCTOBER-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Wilhem F. Gadiano, Esq.

; REGISTRATION NUMBER: 37,136

; REFERENCE/DOCKET NUMBER: 4121-40

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-429-0625

; TELEFAX: (202) 293-1850

; TELEX: 650 383-5605

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 81 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-470-953A-27

; Query Match 100.0%; Score 81; DB 3; Length 81;

; Best Local Similarity 100.0%; Pred. No. 1.8e-19;

; Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 ATGAATTTGAAAGATTGAGGCTGTTGTTGATGATGATTTGGATTGCTGACACTG 60

; DB 1 ATGAATTTGAAAGATTGAGGCTGTTGTTGATGATGATTTGGATTGCTGACACTG 60

; QY 61 ACGGCTGTGCCGCTCATGCG 81

; DB 61 ACGGCTGTGCCGCTCATGCG 81

RESULT 4

US-08-470-953A-28

; Sequence 28, Application US/08470953A

; Patent No. 6346407

; GENERAL INFORMATION:

APPLICANT: ANDREE LAHAYE
 APPLICANT: ERIC DE BUYL
 APPLICANT: PIERRE LEDOUX
 APPLICANT: RENE DETROZ
 TITLE OF INVENTION: Xylanase, microorganisms produced it,
 TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
 TITLE OF INVENTION: and uses thereof
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
 STREET: 2000 K St., N.W., Suite 200
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM: disk
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,953A
 FILING DATE: 6-OCTOBER-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilhem F. Gadiano, Esq.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-40
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-429-0625
 TELEFAX: (202) 293-1850
 TELEX: 650 383-5605
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 81 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..81
 US-08-470-953A-28
 Query Match 100.0%; Score 81; DB 3; Length 81;
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAATTGAAAGATTGAGCTGTTGTTGTGATGTGATTTGCTGACTG 60
 Db 1 ATGAATTGAAAGATTGAGCTGTTGTTGTGATGTGATTTGCTGACTG 60
 QY 61 ACGGCTGCGGCTCATGCG 81
 Db 61 ACGGCTGCGGCTCATGCG 81
 RESULT 5
 US-09-076-677-27
 Sequence 27, Application US/09076677
 Patent No. 6423523
 GENERAL INFORMATION:
 APPLICANT: DE BUYL, ERIC
 LAHAYE, ANDREE
 LEDOUX, PIERRE
 AMORY, ANTOINE
 DETROZ, RENE
 ANDRE, CHRISTOPHE
 VETTER, ROMAN
 TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
 EXPRESSION VECTORS FOR SUCH XYLANASE AND
 OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 USE THEREOF

EXPRESSION VECTORS FOR SUCH XYLANASE AND
 OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 USE THEREOF
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
 STREET: 2000 K St., N.W., Suite 200
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM: disk
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/076,677
 FILING DATE: 12-May-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/275,526
 FILING DATE: 15-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Gadiano, Wilhem F.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-49
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 429-0625
 TELEFAX: (202) 293-0625
 TELEX: 650 383 5605
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 81 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-09-076-677-27
 Query Match 100.0%; Score 81; DB 4; Length 81;
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;
 Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAATTGAAAGATTGAGCTGTTGTTGTGATGTGATTTGCTGACTG 60
 Db 1 ATGAATTGAAAGATTGAGCTGTTGTTGTGATGTGATTTGCTGACTG 60
 QY 61 ACGGCTGCGGCTCATGCG 81
 Db 61 ACGGCTGCGGCTCATGCG 81
 RESULT 6
 US-09-076-677-33
 Sequence 33, Application US/09076677
 Patent No. 6423523
 GENERAL INFORMATION:
 APPLICANT: DE BUYL, ERIC
 LAHAYE, ANDREE
 LEDOUX, PIERRE
 AMORY, ANTOINE
 DETROZ, RENE
 ANDRE, CHRISTOPHE
 VETTER, ROMAN
 TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
 EXPRESSION VECTORS FOR SUCH XYLANASE AND
 OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 USE THEREOF
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.

```

; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,677
; FILING DATE: 12-May-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,526
; FILING DATE: 15-JUL-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
;
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-076-677-33

Query Match 100.0%; Score 81; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTGAAAAGATTGAGGCTGTTGTTGGATGTGATTTGGATTGTTGCTGACACTG 60
Db 1 ATGAATTGAAAAGATTGAGGCTGTTGTTGGATGTGATTTGGATTGTTGCTGACACTG 60

QY 61 ACGGCTGCCGGCTCATCG 81
Db 61 ACGGCTGCCGGCTCATCG 81

RESULT 7
US-09-073-055-27
; Sequence 27, Application US/09073055
; Patent No. 6426211
;
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; LAHAYE, ANDR E
; LEDOUX, PIERRE
; AMORY, ANTOINE
; DETROZ, REN
; ANDRE, CHRISTOPHE
; VETTER, ROMAN
;
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; EXPRESSION VECTORS FOR SUCH XYLANASE AND
; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; USE THEREOF
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
;
; COUNTRY: U.S.A.
; ZIP: 20006
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,055
; FILING DATE: 05-May-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,526
; FILING DATE: 15-JUL-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
;
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-073-055-27

Query Match 100.0%; Score 81; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTGAAAAGATTGAGGCTGTTGTTGGATGTGATTTGGATTGTTGCTGACACTG 60
Db 1 ATGAATTGAAAAGATTGAGGCTGTTGTTGGATGTGATTTGGATTGTTGCTGACACTG 60

QY 61 ACGGCTGCCGGCTCATCG 81
Db 61 ACGGCTGCCGGCTCATCG 81

RESULT 8
US-09-073-055-33
; Sequence 33, Application US/09073055
; Patent No. 6426211
;
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; LAHAYE, ANDR E
; LEDOUX, PIERRE
; AMORY, ANTOINE
; DETROZ, REN
; ANDRE, CHRISTOPHE
; VETTER, ROMAN
;
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; EXPRESSION VECTORS FOR SUCH XYLANASE AND
; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; USE THEREOF
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
;
; COUNTRY: U.S.A.
; ZIP: 20006
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,055
; FILING DATE: 05-May-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,526
; FILING DATE: 15-JUL-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
;
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-073-055-27
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/073.055
  FILING DATE: 05-May-1998
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/275.526
  FILING DATE: 15-JUL-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Gadiano, Wilhlem F.
  REGISTRATION NUMBER: 37,136
  REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 429-0625
  TELEFAX: (202) 293-0625
  TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 33:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 81 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: genomic DNA
  ORIGINAL SOURCE:
    ORGANISM: Bacillus pumilus
    STRAIN: PRL B12
  SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-073-055-33
Query Match      100.08; Score 81; DB 4; Length 81;
Best Local Similarity 100.08; Pred. No. 1.8e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0;
QY      1 ATGAATTGAAAAGATTGAGGCTGTTTGTGATGTGATTGGATTGTGCTGCTGA
Ddb     1 ATGAATTGAAAAGATTGAGGCTGTTTGTGATGTGATTGGATTGTGCTGCTGA
QY      61 ACGGCTGTGCCGGCTCATGCG 81
Ddb     61 ACGGCTGTGCCGGCTCATGCG 81
RESULT 9
US-08-275-526C-30
  Sequence 30, Application US/08275526C
  Patent No. 6180382
  GENERAL INFORMATION:
    APPLICANT: DE BUYL, ERIC
    APPLICANT: LAHAYE, ANDR E
    APPLICANT: LEDOUX, PIERRE
    APPLICANT: AMORY, ANTOINE
    APPLICANT: DETROZ, REN
    APPLICANT: ANDRE, CHRISTOPHE
    APPLICANT: VETTER, ROMAN
  TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
  TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
  TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREOF AND
  TITLE OF INVENTION: USE THEREOF
  NUMBER OF SEQUENCES: 35
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
    STREET: 2000 K St., N.W., Suite 200
    CITY: Washington
    STATE: D.C.
    COUNTRY: U.S.A.
    ZIP: 20006
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/275.526C

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RESULT 9
US-08-275-526C-30
Sequence 30, Application US/08275526C
Patent No. 6180382
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
APPLICANT: LAHAVE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: DETROZ, REN
APPLICANT: ANDRE, CHRISTOPHE
APPLICANT: VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275-526C

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; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-08-275-526C-30

Query Match 100.0%; Score 81; DB 3; Length 681;
Best Local Similarity 100.0%; Pred. No. 3.8e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 ATGAATTTGAAAGATTGAGCGCTGTTGTTTGTGATGTGATTGGATTTCGTCTGACACTG 60
DB 1 ATGAATTTGAAAGATTGAGCGCTGTTGTTTGTGATGTGATTGGATTTCGTCTGACACTG 60

QY 61 ACGGCTGTCCGGCTCATGCG 81
DB 61 ACGGCTGTCCGGCTCATGCG 81

RESULT 10
US-08-275-526C-32
; Sequence 32, Application US/08275526C
; Patent No. 6180382
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: LAHAYE, ANDR E
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE
; APPLICANT: DETROZ, REN
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,526C
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605

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;
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
; US-08-275-526C-32

Query Match          100.0%; Score 81; DB 3; Length 681;
Best Local Similarity 100.0%; Pred. No. 3.8e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGTGATTTGATTTGCTGACACTG 60
Db 1 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGTGATTTGATTTGCTGACACTG 60

QY 61 ACGGCTGTGCCGCTCATCG 81
Db 61 ACGGCTGTGCCGCTCATCG 81

RESULT 11
US-09-076-677-30
; Sequence 30, Application US/09076677
; Patent No. 6423523
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; LAHAYE, ANDREE
; LEDOUX, PIERRE
; AMORY, ANTOINE
; DETROZ, RENE
; ANDRE, CHRISTOPHE
; VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; EXPRESSION VECTORS FOR SUCH XYLANASE AND
; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,677
; FILING DATE: 12-May-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,526
; FILING DATE: 15-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
; US-09-076-677-30

;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Query Match          100.0%; Score 81; DB 4; Length 681;
Best Local Similarity 100.0%; Pred. No. 3.8e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGTGATTTGATTTGCTGACACTG 60
Db 1 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGTGATTTGATTTGCTGACACTG 60

QY 61 ACGGCTGTGCCGCTCATCG 81
Db 61 ACGGCTGTGCCGCTCATCG 81

RESULT 12
US-09-076-677-32
; Sequence 32, Application US/09076677
; Patent No. 6423523
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; LAHAYE, ANDREE
; LEDOUX, PIERRE
; AMORY, ANTOINE
; DETROZ, RENE
; ANDRE, CHRISTOPHE
; VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; EXPRESSION VECTORS FOR SUCH XYLANASE AND
; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,677
; FILING DATE: 12-May-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,526
; FILING DATE: 15-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
```


Db 1 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGCTGATTGGATTGTTGCTGACACTG 60
QY 61 ACGGCTGTGCCGGCTCATGCG 81
Db 61 ACGGCTGTGCCGGCTCATGCG 81

RESULT 15
US-08-275-526C-1
; Sequence 1, Application US/08275526C
; Patent No. 6180382
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: LAHAYE, ANDR E
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE
; APPLICANT: DETROZ, REN
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND,
; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,526C
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
; US-08-275-526C-1

Query Match 100.0%; Score 81; DB 3; Length 1022;
Best Local Similarity 100.0%; Pred. No. 4.3e-19;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGCTGATTGGATTGTTGCTGACACTG 60
Db 186 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGCTGATTGGATTGTTGCTGACACTG 245
QY 61 ACGGCTGTGCCGGCTCATGCG 81
Db 246 ACGGCTGTGCCGGCTCATGCG 266

Search completed: November 11, 2004, 01:34:29
Job time : 11.3051 secs


```

; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-909-207-27

Query Match 100.0%; Score 81; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTGAAAAGATTGAGGCTGTGTTGTGATGCTGATTGCGTCTGCTGACACTG 60
Db 1 ATGAATTGAAAAGATTGAGGCTGTGTTGTGATGCTGATTGCGTCTGCTGACACTG 60

QY 61 ACGGCTGTCCGGCTCATCG 81
Db 61 ACGGCTGTCCGGCTCATCG 81

RESULT 2
US-09-909-207-28
; Sequence 28, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSER: WILLIAM BRINKS HOPFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,207
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..81
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-909-207-28

Query Match 100.0%; Score 81; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTGAAAAGATTGAGGCTGTGTTGTGATGCTGATTGCGTCTGCTGACACTG 60
Db 1 ATGAATTGAAAAGATTGAGGCTGTGTTGTGATGCTGATTGCGTCTGCTGACACTG 60

QY 61 ACGGCTGTCCGGCTCATCG 81
Db 61 ACGGCTGTCCGGCTCATCG 81

RESULT 3
US-09-770-961-259/c
; Sequence 259, Application US/09770961
; Publication No. US20030115639A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Kameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieger, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hubban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2026 (PARA-015PRV)
; CURRENT APPLICATION NUMBER: US/09/770,961
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,466
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-961-259

Query Match 36.3%; Score 29.4; DB 10; Length 508;
Best Local Similarity 70.9%; Pred. No. 6.5;
Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGAATTGAAAAGATTGAGGCTGTGTTGTGATGCTGATTGCGTCTGCTGACACTG 55
Db 159 ATGCATGTGTAAAGCTTGATGATGCTTTGTTGTGCTCTGGATTGCTGCTGACACTG 105

RESULT 4
US-10-027-632-263227
; Sequence 263227, Application US/10027632
; Publication No. US20020198371A1

```



```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 263227
: LENGTH: 2363
: TYPE: DNA
: ORGANISM: Human
: US-10-027-632-263227

```

Query Match	35.8%	Score 29;	DB 13;	Length 2363;
Best Local Similarity	67.2%	Pred. No. 15;		
Matches 41;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;

QY	1	ATGAATTTGAAAGATTGAGCGTGTGTTTGTGATGCTGATTGGATTGTGCTGCACACTG	60
Db	1219	ATGCATCTTATTAGATGAGAAATGTTGTAGATAATGATTATATGTTTGTCTCGAGATTG	1278
QY	61	A 61	
		—	
Db	1279	A 1279	

```

RESULT 5
US-10-027-632-263228
; Sequence 263228, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263228
; LENGTH: 2363
; TYPE: DNA
; ORGANISM: Human

```

```

US-10-027-632-263228

Query Match          35.8%; Score 29; DB 13; Length 2363;
Best Local Similarity 67.2%; Pred. No. 15;
Matches 41; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy      1  ATGAATTGAAAAGATTGAGCGCTGTTGTTGTGTCATGCTGTATTGGATTTCGTCTGACACTG 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1219 ATGCATCTTATTAGAATGAGAATGTTGTAGATAATGATTATATATGGTTTGTCTCGAGATTG 1278

Qy      61  A 61
      |
Db 1279 A 1279

```

```

RESULT 6
US-10-027-632-263227
; Sequence 263227, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 263227
; LENGTH: 2363
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-263227

```

Query Match	35.8%	Score 29;	DB 15;	Length 2363;
Best Local Similarity	67.2%;	Pred. No. 15;		
Matches 41;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;

Qy	1	ATGAATTGAAAGATTGAGCGTGTGTTTGTGATGTGTAATGGATTGCTGCACACTG	60
Db	1219	ATGCATCTTATTAGAATGAGAATGTTCTAGATAATGATTAATGGTTTGCTCGAGATTG	1278
Qy	61	A 61	
Db	1279	A 1279	

```

RESULT 7
US-10-027-632-263228
; Sequence 263228, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006

```

	Query Match	35.6%;	Score 28.8;	DB 13;	Length 233060;	
	Best Local Similarity	62.5%;	Pred. No. 81;			
	Matches	45;	Conservative	0;	Mismatches	27;
					Indels	0;
	Gaps	0;				
Qy	5	ATTGTAAAGATTGAGCGCTGTTTGTTCATGCTGTATTGGATTGCTGCACACTGACGG	64			
Dd	102441	ATTTGCTTTCCATCATGAGCAAGTTGTGATGTGGATGCCAGTTCTGGTGCAGTGTCTCAG	102500			
Qy	65	CTGTGCCGGCTC	76			
Dd	102501	CTTAGCTGGCTC	102512			

Query Match 34.5%; Score 28; DB 13; Length 87731;
Best Local Similarity 63.2%; Pred. NO. 1.1e+02;
Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 5 ATTGAAAGATGAGGCTGTTCTGCTGATGTATTGGATTGTGCTGACACTGACGG 64
|||||

Db 70914 ATATGAAGGGCTGAGGCTAGTGTCTCTTTAAATAGATCAGTTCCCACTGTGTCT 70855

QY 65 CTGTGCG 72

Db 70854 CTGGGCTG 70847

RESULT 11

US-10-425-115-162687/c
; Sequence 162687, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 162687
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_79947C.1
US-10-425-115-162687

Query Match 34.1%; Score 27.6; DB 18; Length 614;
Best Local Similarity 60.8%; Pred. No. 28;
Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 8 TGAAGAAGATTGAGGCTGTTCTTTGTGATGTATGTGATTTGTGCTGACACTGACGGCTG 67

Db 189 TGTATGATGGTGATCTCCACACGGTGATGTCGATGGTTTGTCTGAGGAAGGGCGG 130

QY 68 TGCCGGCTCATGG 81

Db 129 TGTAGGATCAGGCG 116

RESULT 12

US-10-425-115-137066
; Sequence 137066, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 137066
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_56480C.1
US-10-425-115-137066

Query Match 34.1%; Score 27.6; DB 18; Length 1383;
Best Local Similarity 78.6%; Pred. No. 37;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 ATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTGTTTGGAT 46

Db 1290 ATATGACAGATGAAGACTGTGTTGTGATATATGTTGGAT 1331

RESULT 13

US-10-425-115-83971/c
; Sequence 83971, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 83971
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_176594C.1
US-10-425-115-83971

Query Match 33.8%; Score 27.4; DB 18; Length 263;
Best Local Similarity 75.6%; Pred. No. 25;
Matches 34; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 6 TTTGAAAAGATTGAGGCTGTTCTTTGTGATGTATGTGATTTGT 50

Db 194 TTAGAATAGATTGAAGCTGCTGTGTGTGTTCTGTATGT 150

RESULT 14

US-10-437-963-16223/c
; Sequence 16223, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 16223
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21993C.1
US-10-437-963-16223

Query Match 33.8%; Score 27.4; DB 17; Length 648;
Best Local Similarity 62.3%; Pred. No. 33;
Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 ATGAATTTGAAAAGATTGAGGCTGTTCTTTGTGATGTATGTGATTTGTGCTGACACTG 60

Db 101 ATGTTTTTGGAATAAATTTTGTGAGGATGTTATGAATGATCTGTAATGTCATT 42

QY 61 ACGGCTGTG 69

Db 41 AGATCTGTG 33

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RESULT 15
US-10-437-963-71944
; Sequence 71944, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 71944
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72369C.1
US-10-437-963-71944

Query Match      33.8%; Score 27.4; DB 17; Length 1763;
Best Local Similarity 75.6%; Pred. No. 47;
Matches 34; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY      4 AATTGAAAGATTGAGGCTGTTGTTGATGATGATGATTT 48
Db      1348 AAGATGAAAGATGATGATGATGATGATGATTTGTTGATTTGATTTGATTT 1392

Search completed: November 11, 2004, 02:08:35
Job time : 55.7881 secs.
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 17:09:58 ; Search time 76.1638 Seconds
(without alignments)
6187.359 Million cell updates/sec

Title: US-09-909-207-1
Perfect score: 663
Sequence: 1 CAATCGTCACGACAAATTC.....TAACCTTCGATAAACAAAT 663

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/prodata/1/ina/5B_COMB.seq:
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:
6: /cgn2_6/prodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	663	3	US-08-470-953A-1
2	663	100.0	663	3	US-08-470-953A-2
3	663	100.0	744	3	US-08-470-953A-4
4	663	100.0	744	3	US-08-470-953A-5
5	663	100.0	1513	3	US-08-470-953A-10
6	663	100.0	1513	3	US-08-470-953A-11
7	634.2	95.7	744	1	US-09-189-060B-1
8	634.2	95.7	871	1	US-08-698-978-1
9	624.6	94.2	744	3	US-08-501-126-18
10	507.8	76.6	744	3	US-09-189-060B-11
11	255.4	38.5	2364	3	US-09-390-234-23
12	255.4	38.5	2364	4	US-09-603-311-23
13	255.2	38.5	1022	3	US-08-275-526C-1
14	255.2	38.5	1022	3	US-08-275-526C-35
15	255.2	38.5	1022	4	US-09-076-677-1
16	255.2	38.5	1022	4	US-09-076-677-35
17	255.2	38.5	1022	4	US-09-073-055-1
18	255.2	38.5	1022	4	US-09-073-055-35
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20	255	38.5	600	4	US-08-275-526C-34
21	255	38.5	600	4	US-09-076-677-26
22	255	38.5	600	4	US-09-076-677-34
23	255	38.5	600	4	US-09-073-055-26
24	255	38.5	600	4	US-09-073-055-34
25	255	38.5	681	3	US-08-275-526C-30
26	255	38.5	681	3	US-08-275-526C-32
27	255	38.5	681	4	US-09-076-677-30

28	255	38.5	681	4	US-09-076-677-32
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30	255	38.5	681	4	US-09-073-055-32
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32	154.4	23.3	164	3	US-08-501-126-15
33	154.4	23.3	164	3	US-08-501-126-16
34	132.4	20.0	294	3	US-08-817-946-4
35	132.4	20.0	294	4	US-09-639-354A-4
36	119.4	18.0	1375	2	US-08-468-812-1
37	119.4	18.0	1375	3	US-08-590-563-1
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39	119.4	18.0	1375	4	US-09-235-832-1
40	119	17.9	229	3	US-09-189-060B-53
41	118.4	17.9	573	1	US-08-709-912-18
42	118.4	17.9	573	2	US-09-047-370-18
43	117.8	17.8	1207	1	US-08-575-964-2
44	117.8	17.8	1207	2	US-08-963-500-2
45	115.2	17.4	213	3	US-09-189-060B-49

ALIGNMENTS

RESULT 1
US-08-470-953A-1
Sequence 1, Application US/08470953A
Patent No. 6346407

GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
APPLICANT: ERIC DE BUYL
APPLICANT: PIERRE LEDOUX
APPLICANT: RENE DETROZ
TITLE OF INVENTION: xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
US-08-470-953A-1

ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,953A
 FILING DATE: 6-OCTOBER-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilhem F. Gadiano, Esq.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-40
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-429-0625
 TELEFAX: (202) 293-1850
 TELEX: 650 383-5605
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 663 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 STRAIN: Bacillus
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 1..663
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..663
 US-08-470-953A-2

Query Match	100.0%;	Score 663;	DB 3;	Length 663;
Best Local Similarity	100.0%;	Pred. No. 7.9e-198;		
Matches 663;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	61	GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGGTACGTT	CAGTTCAGTTCAGTTCGCCAATGG	120
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QY	121	AACAAATGTTAAACAACATATTTATTTCCGTAAGGTAAAAAATTC	CAATTTGAAACACAAACACAC	180
Db	121	AACAAATGTTAAACAACATATTTATTTCCGTAAGGTAAAAAATTC	CAATTTGAAACACAAACACAC	180
QY	181	CAACAAGTTGGTAACATGTCCTATAAACAATAGCGGACCACTTCC	CAACCAAAATGGTAATGCG	240
Db	181	CAACAAGTTGGTAACATGTCCTATAAACAATAGCGGACCACTTCC	CAACCAAAATGGTAATGCG	240
QY	241	TATTTATGCGTCTATGTTGGACGTGTGGACCTCTTGTCGAATATTTAT	TATTTGTCGACAGT	300
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Db	301	TGGGGCAACTGGCGTCCACAGGAGCAACGCCCTTAAGGGGACCAT	CATCACTGTTGATGGAGGA	360
QY	361	ACATATGATCTACGAGAGCTCTTAGAGTCAATCAACCCCTCCATTTA	AGGGGATTCGCCACA	420
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QY	421	TTTTAAACAATATTCGAGTGTTCGAAAGATCGAAACGCAACGAGTGG	CACGATTTCTGTCAAC	480
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Query Match 100.0%; Score 663; DB 3; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.9e-198;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CAAATCGTCACCGACAATTCCTATTTGGGCAACACACGATGGCTATGATATGAAATTTTGGAAA 60
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61 GATACGGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTAGCTTCAGTGCCTCAATGG 120
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61 GATACGGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTAGCTTCAGTGCCTCAATGG 120
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121 AACAAATGTTAAACACATATTTATTCGGTAAAGGTAAATAAATTCATGAAACACAAACACAC 180
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181 CAACAAGTTGGTAAATGCTCCATAAACTACCGAGCCAACTTCCAAACCAAAATGGTAATGCG 240
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181 CAACAAGTTGGTAAATGCTCCATAAACTACCGAGCCAACTTCCAAACCAAAATGGTAATGCG 240
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241 TATTATTCGGTCTATGTTGGGACATGTTGACCCCTCTTGTGCAATATTAATTTGTGACAGT 300
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301 TGGGGCAACTGGCGTCCACAGGACACGCTTAAGGGGACCATCACCTGTTGATGGAGGA 360
|||
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|||
361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGGATGCCCACA 420
|||
361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGGATGCCCACA 420
|||
421 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAAACGACAGTGGCACGATTTCTGTCAGC 480
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421 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAAACGACAGTGGCACGATTTCTGTCAGC 480
|||
481 AACCACCTTTAGNGCGTGGGAAAACCTTAGGGATGAATATGGGAAAATGTATGAAGTCGCG 540
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481 AACCACCTTTAGNGCGTGGGAAAACCTTAGGGATGAATATGGGAAAATGTATGAAGTCGCG 540
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541 CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGTCTAATGTATATAGCAATACATAAGA 600
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541 CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGTCTAATGTATATAGCAATACATAAGA 600
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601 ATTAACGGTAACCCCTCTCTCAACTATTAGTAAATGACGAGACATTAACCTTTGATATAAAC 660
|||
601 ATTAACGGTAACCCCTCTCTCAACTATTAGTAAATGACGAGACATTAACCTTTGATATAAAC 660
|||

661 AAT 663
661 AAT 663

RESULT 2
US-08-470-953A-2
; Sequence 2, Application US/08470953A
; Patent No. 634607
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; APPLICANT: ERIC DE BUYL
; APPLICANT: PIERRE LEDOUX
; APPLICANT: RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
; TITLE OF INVENTION: and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.

App!

481 AACCACTTTAGAGCGTGGGAAACTTAGGATGAATATGGGAAATATGATGAAGTCGCG 540
 481 AACCACTTTAGAGCGTGGGAAACTTAGGATGAATATGGGAAATATGATGAAGTCGCG 540
 541 CTTACTGTAGAGCGTCTCAACTATTAGTAATGAGCGAGCATTAATTTGGATAAAC 600
 541 CTTACTGTAGAGCGTCTCAACTATTAGTAATGAGCGAGCATTAATTTGGATAAAC 600
 601 ATTAACGGTAAACCTCTCTCAACTATTAGTAATGAGCGAGCATTAATTTGGATAAAC 660
 601 ATTAACGGTAAACCTCTCTCAACTATTAGTAATGAGCGAGCATTAATTTGGATAAAC 660
 661 AAT 663
 661 AAT 663

RESULT 3
 US-08-470-953A-4
 ; Sequence 4, Application US/08470953A
 ; Patent No. 6346407
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDREE LAHAYE
 ; APPLICANT: ERIC DE BUYL
 ; APPLICANT: PIERRE LEDOUX
 ; APPLICANT: RENE DETROZ
 ; TITLE OF INVENTION: Xylanase, microorganisms produced it,
 ; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
 ; TITLE OF INVENTION: and uses thereof
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOPFER GILSON & LIONE
 ; STREET: 2000 K St., N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,953A
 ; FILING DATE: 6-OCTOBER-1995
 ; CLASSIFICATION: 435
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilhem F. Gadiano, Esq.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-40
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-429-0625
 ; TELEFAX: (202) 293-1850
 ; TELEX: 650 383-5605
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 744 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; STRAIN: Bacillus

US-08-470-953A-4
 Query Match 100.0%; Score 663; DB 3; Length 744;
 Best Local Similarity 100.0%; Pred. No. 8.4e-198;
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 61 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGCGGCTAGCTTCAAGTCCCAATGG 120
 142 GATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGCGGCTAGCTTCAAGTCCCAATGG 201
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 202 AACATGTTTAAACACATATTATTCGTAAGAGTAAATAATCAATGAACACACACACAC 261
 181 CAACAAGTTGGTAAACATGTCATATAAATACGAGCAACCTTCCAAACCAACCAATGG 240
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 241 TATTTATCGGTCTATGGTTGACTGTTGACCTCTTGTGCAATATATATTTGTCGACAGT 300
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 301 TGGGCAACTGGCGTCCACAGGAGCAACGCCCTAAGGGGACCATCACTGTTGATGGAGGA 360
 382 TGGGCAACTGGCGTCCACAGGAGCAACGCCCTAAGGGGACCATCACTGTTGATGGAGGA 441
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 442 ACATATGATATCTACGAGACTTTAGAGTCAATCAACCTCCATTAAGGGGATTTGCCACA 501
 421 TTTAAACAATATTTGAGTGTTCGAAGATCGAAGCCGAGTGGGACGATTTCTGTCAGC 480
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 481 AACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATGGGAAATATGATGAAGTCGCG 540
 562 AACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATGGGAAATATGATGAAGTCGCG 621
 541 CTTACTGTAGAGCGTCTCAACTATTAGTAATGAGCGAGCATTAATTTGGATAAAC 600
 622 CTTACTGTAGAGCGTCTCAACTATTAGTAATGAGCGAGCATTAATTTGGATAAAC 681
 601 ATTAACGGTAAACCTCTCTCAACTATTAGTAATGAGCGAGCATTAATTTGGATAAAC 660
 682 ATTAACGGTAAACCTCTCTCAACTATTAGTAATGAGCGAGCATTAATTTGGATAAAC 741
 661 AAT 663
 742 AAT 744

RESULT 4
 US-08-470-953A-5
 ; Sequence 5, Application US/08470953A
 ; Patent No. 6346407
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDREE LAHAYE
 ; APPLICANT: ERIC DE BUYL
 ; APPLICANT: PIERRE LEDOUX
 ; APPLICANT: RENE DETROZ
 ; TITLE OF INVENTION: Xylanase, microorganisms produced it,
 ; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
 ; TITLE OF INVENTION: and uses thereof
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOPFER GILSON & LIONE
 ; STREET: 2000 K St., N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: IBM PC compatible
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; FILING DATE: 6-OCTOBER-1995
 ; CLASSIFICATION: 435
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilhem F. Gadiano, Esq.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-40
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-429-0625
 ; TELEFAX: (202) 293-1850
 ; TELEX: 650 383-5605
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 744 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; STRAIN: Bacillus

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 82..744
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..81
US-08-470-953A-5

Query Match 100.0%; Score 663; DB 3; Length 744;
Best Local Similarity 100.0%; Pred. No. 8.4e-198; Indels 0; Gaps 0;
Matches 663; Conservative 0; Mismatches 0;

QY 1 CAAATCGTCCAGCAATTCATGGCAACACGATGGCTATGATTGAATTTGGAAA 60
DB 82 CAAATCGTCCAGCAATTCATGGCAACACGATGGCTATGATTGAATTTGGAAA 141
QY 61 GATAGCGGTGGCTCTGGGCAATGATCTCAATCATGCGGTACGTTCAAGTCCCAATGG 120
DB 142 GATAGCGGTGGCTCTGGGCAATGATCTCAATCATGCGGTACGTTCAAGTCCCAATGG 201
QY 121 AACAAATGTTAAACAATATTTATTCCTGTAAGGTAAATAATTCATGAAACACAAACACAC 180
DB 202 AACAAATGTTAAACAATATTTATTCCTGTAAGGTAAATAATTCATGAAACACAAACACAC 261
QY 181 CAACAAATGTTAAACAATGTCATTAATACTACGGAGCAACCTTCCAAACCAATGTTAATGGC 240
DB 262 CAACAAATGTTAAACAATGTCATTAATACTACGGAGCAACCTTCCAAACCAATGTTAATGGC 321
QY 241 TATTATGCTCTATGTTGAGCTGTTGACCTCTTGTGCAATATTATTTGCGACAGT 300
DB 322 TATTATGCTCTATGTTGAGCTGTTGACCTCTTGTGCAATATTATTTGCGACAGT 381
QY 301 TGGGGCAACTGGGGTCCACAGGAGCAACCGCTTAAGGGACCAATCACTGTTGATGAGGA 360
DB 382 TGGGGCAACTGGGGTCCACAGGAGCAACCGCTTAAGGGACCAATCACTGTTGATGAGGA 441
QY 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGATGTCACCA 420
DB 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGATGTCACCA 501
QY 421 TTTTAAACAATTTGAGGTGTTGCAAGATCGAAACGACGAGTGGCAGATTTCTGTGAGC 480
DB 502 TTTTAAACAATTTGAGGTGTTGCAAGATCGAAACGACGAGTGGCAGATTTCTGTGAGC 561
QY 481 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATGGGAAAATGATGAAGTCGCG 540

DB 562 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATGGGAAAATGATGAAGTCGCG 621
QY 541 CTTACTGTAGAAGGCTATCAAAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 600
DB 622 CTTACTGTAGAAGGCTATCAAAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 681
QY 601 ATTAACGGTAAACCTCTCTCAACTATTAGTATAGCAGAGCATAACTTTGGATAAAAAAC 660
DB 682 ATTAACGGTAAACCTCTCTCAACTATTAGTATAGCAGAGCATAACTTTGGATAAAAAAC 741
QY 661 AAT 663
DB 742 AAT 744
RESULT 5
US-08-470-953A-10
Sequence 10, Application US/08470953A
Patent No. 6346407
GENERAL INFORMATION:
APPLICANT: ANDRES LAHAYE
APPLICANT: ERIC DE BUHL
APPLICANT: PIERRE LEDOUX
APPLICANT: RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C. U.S.A.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/470,953A
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
US-08-470-953A-10

Query Match 100.0%; Score 663; DB 3; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.2e-197; Indels 0; Gaps 0;
Matches 663; Conservative 0; Mismatches 0;
QY 1 CAAATCGTCCAGCAATTCATGGCAACACGATGGCTATGATTGAATTTGGAAA 60

QY 541 CTTACTGTAGAGGCTATCAAGTAGCGAAGTCTAATGTATATAGCAATACACTAAGA 600
DB 1241 CTTACTGTAGAGGCTATCAAGTAGCGAAGTCTAATGTATATAGCAATACACTAAGA 1300
QY 601 ATTACGGTAAACCTCTCTCAACTATTATAGTATACAGGAGCATAACTTTGGATAAAAC 660
DB 1301 ATTACGGTAAACCTCTCTCAACTATTATAGTATACAGGAGCATAACTTTGGATAAAAC 1360
QY 661 AAT 663
DB 1361 AAT 1363

RESULT 7
US-09-189-060B-1
; Sequence 1, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Bacillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(744)
US-09-189-060B-1

Query Match 95.7%; Score 634.2; DB 3; Length 744;
Best Local Similarity 97.3%; Pred. No. 8.9e-189;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 CAAATCGTCACGACAATTCATTTGGCAACACGATGGCTATGATTAATTTGGAAA 60
DB 82 CAAATCGTCACGACAATTCATTTGGCAACACGATGGCTATGATTAATTTGGAAA 141
QY 61 GATAGCGGTGGCTCTGGGACAATGATTCATCATGCGGTACGTTCAAGTCCCAATGG 120
DB 142 GATAGCGGTGGCTCTGGGACAATGATTCATCATGCGGTACGTTCAAGTCCCAATGG 201
QY 121 AACAAATGTTAAACAATATTTATTCGTAAGGTAAATAATCAATGAACACAAACACAC 180
DB 202 AACAAATGTTAAACAATATTTATTCGTAAGGTAAATAATCAATGAACACAAACACAC 261
QY 181 CAACAAGTTGGTAACATGTCATTAACACTACGAGCCAACTTCCAAACCAATGTAATGG 240
DB 262 CAACAAGTTGGTAACATGTCATTAACACTACGAGCCAACTTCCAAACCAATGTAATGG 321
QY 241 TATTTATGCGTCTATGTTGGACTGTGACCTCTTGTGCAATATTATTTGTCGACAT 300
DB 322 TATTTATGCGTCTATGTTGGACTGTGACCTCTTGTGCAATATTATTTGTCGATAGT 381
QY 301 TGGGGCAACTGGCGTCCACAGAGCAACGCCCTTAAGGGACCAATCACTGTTGATGAGGA 360
DB 382 TGGGGCAACTGGCGTCCACAGAGCAACGCCCTTAAGGGACCAATCACTGTTGATGAGGA 441
QY 361 ACATATGATATACAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGATTGCCACA 420
DB 442 ACATATGATATATATGATTAATCTTTAGAGTCAATCAACCCCTCCATTAAAGGGATTGCCACA 501
QY 421 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCCAGATTTCTGTGACG 480

DB 502 TTTAAACAATATTGGAGTGTCCGAGATCGAARACGACGAGTGGCACAATTTCTGTGACG 561
QY 481 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATCGGGAATAATGTATGAAGTCGCG 540
DB 562 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATCGGGAATAATGTATGAAGTCGCG 621
QY 541 CTTACTGTAGAGGCTATCAAGTAGCGAAGTCTAATGTATATAGCAATACACTAAGA 600
DB 622 CTTACTGTAGAGGCTATCAAGTAGCGAAGTCTAATGTATATAGCAATACACTAAGA 681
QY 601 ATTACGGTAAACCTCTCTCAACTATTATAGTATACAGGAGCATAACTTTGGATAAAAC 660
DB 682 ATTACGGTAAACCTCTCTCAACTATTATAGTATACAGGAGCATAACTCTAGATAAAAC 741
QY 661 AAT 663
DB 742 AAT 744

RESULT 8
US-08-698-978-1
; Sequence 1, Application US/08698978
; Patent No. 5770424
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Danbmann, Claus
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Sch lein, Martin
; APPLICANT: Jorgensen, Per Linnaa
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS OF PRODUCING
; TITLE OF INVENTION: XYLANOLYTIC ENZYMES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: NO. 57704240 No. 5770424disk of No. 5770424th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/698,978
; FILING DATE: 16 August 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,398
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/343,600
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK93/00218
; FILING DATE: 2-JUL-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeca A.
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 3794.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:
ORGANISM: Bacillus agaradherens
STRAIN: NCIMB 40482
FEATURE:
NAME/KEY: CDS
LOCATION: 82..744
US-08-698-978-1

Query Match 95.7%; Score 634.2; DB 1; Length 871;
Best Local Similarity 97.3%; Pred. No. 9.7e-189;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 CAAATCGTCACCGACAAATCCATTTGGCAACACGATGGCTATGATTATGAATTTGGAAA 60
DB |||||||
QY 82 CAAATCGTCACCGACAAATTTCCATTTGGCAACACGATGGCTATGATTATGAATTTGGAAA 141
DB |||||||
QY 61 GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGTACGTTCAAGTCCCAATGG 120
DB |||||||
QY 142 GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGTACGTTCAAGTCCCAATGG 201
DB |||||||
QY 121 AACATGTTAAACACATATATTTCCGTAAGGTAAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 180
DB |||||||
QY 202 AACATGTTAAACACATATATTTCCGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 261
DB |||||||
QY 181 CAACAAGTTGGTAACATGTCCTATAAATCAAGGACCACTTCCAAACCAATGTAATGG 240
DB |||||||
QY 262 CAACAAGTTGGTAACATGTCCTATAAATCAAGGACCACTTCCAAACCAATGTAATGG 321
DB |||||||
QY 241 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATATTTATGTCGACAGT 300
DB |||||||
QY 322 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATATTTATGTCGACAGT 381
DB |||||||
QY 301 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGACCACTGCTGTCATGAGGA 360
DB |||||||
QY 382 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGACCACTGCTGTCATGAGGA 441
DB |||||||
QY 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGATTTGCCACA 420
DB |||||||
QY 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGATTTGCCACA 501
DB |||||||
QY 421 TTTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAAGTTCGTCAGC 480
DB |||||||
QY 502 TTTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAAGTTCGTCAGC 561
DB |||||||
QY 481 AACCACTTTAGACGCTGGGAAAACCTTAGGATGAATATGGGGAATATGATGAGTCGG 540
DB |||||||
QY 562 AACCACTTTAGACGCTGGGAAAACCTTAGGATGAATATGGGGAATATGATGAGTCGG 621
DB |||||||
QY 541 CTTACTGTAGAAGCTATCAAGTACGAGTGGTAAATGATATATAGCAATACACTAAGA 600
DB |||||||
QY 622 CTTACTGTAGAAGCTATCAAGTACGAGTGGTAAATGATATATAGCAATACACTAAGA 681
DB |||||||
QY 601 ATTAACGGTAACCCCTCTCTCAACTATTTAGTAATGACGAGAGCAATACTTTGGATATAAAC 660
DB |||||||
QY 682 ATTAACGGTAACCCCTCTCTCAACTATTTAGTAATGACGAGAGCAATACTTTAGATATAAAC 741
DB |||||||
QY 661 AAT 663
DB |||||
QY 742 AAT 744
DB |||||

RESULT 9
US-08-501-126-18
Sequence 18, Application US/08501126
Patent No. 6140095
GENERAL INFORMATION:
APPLICANT: Van Solingen, Pieter
APPLICANT: Williams, Diane P.
APPLICANT: Iverson, Sara
APPLICANT: Farrell, Roberta L.
APPLICANT: Herbes, Wilhelmina T.
APPLICANT: Van Der Kleij, Wilhelmus A.
APPLICANT: Herweijer, Margaretha A.

APPLICANT: Van Beckhoven W.C., Rudolf F.
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Jones, Brian E.
TITLE OF INVENTION: ALKALI-TOLERANT XYLANASES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501.126
FILING DATE: 29-DEC-1995
CLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0057.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
STRAIN: 1-43-3
INDIVIDUAL ISOLATE: CBS672.93
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
OTHER INFORMATION: /product= "xylanase"

US-08-501-126-18
Query Match 94.2%; Score 624.6; DB 3; Length 744;
Best Local Similarity 96.4%; Pred. No. 9.1e-186;
Matches 639; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 CAAATCGTCACCGACAAATTTCCATTTGGCAACACGATGGCTATGATTATGAATTTGGAAA 60
DB |||||||
QY 79 CAAATCGTCACCGACAAATTTCCATTTGGCAACACGATGGCTATGATTATGAATTTGGAAA 138
DB |||||||
QY 61 GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGTACGTTCAAGTCCCAATGG 120
DB |||||||
QY 139 GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGTACGTTCAAGTCCCAATGG 198
DB |||||||
QY 121 AACATGTTAAACACATATATTTCCGTAAGGTAAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 180
DB |||||||
QY 199 AATAATGTTAAACAATATATTTCCGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 258
DB |||||||
QY 181 CAACAAGTTGGTAACATGTCCTATAAATCAAGGACCACTTCCAAACCAATGTAATGCG 240
DB |||||||
QY 259 CAACAAGTTGGTAACATGTCCTATAAATCAAGGACCACTTCCAAACCAATGTAATGCG 318
DB |||||||
QY 241 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATATTTATGTCGACAGT 300
DB |||||||
QY 319 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATATTTATGTCGACAGT 378
DB |||||||
QY 301 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGACCACTGCTGTCATGAGGA 360
DB |||||||
QY 379 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGACCACTGCTGTCATGAGGA 438
DB |||||||

322	TATTATGGCTCTATGGTTGGACTGTTGACCTCTTGTGGAATATATATTGCGATAGT	381
301	TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGA	360
382	TGGGGCAACTGGCGTCCACGAGGGGAACGCTTAAGGGAACATCACTGTTGACGGGGG	441
361	ACATATCATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTGCCACA	420
442	ACGTATGATATCTACAGCACCACACAGGTCAATCAGCCATCTATTAGGGCAGCGCCACC	501
421	TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCCACGAGTGGCACGATTTCTGTCA	480
502	TTCAATCAGTACTGGTTCGATTCCAGAGCAACAGCGGACACGCGGCACCTGTCACTAC	561
481	AACCACTTTAGACGTTGGGAAAACCTTAGGGATGAAATATGGGGAAAACTATGAAAGTC	540
562	AACCACTTTAATGCTGGGCTGCTCTTGCGCATGAAATATGGGTGCAATTCMAATACC	621
541	CTTACTCTGAGAAGCTATCAAGTAGCGGAAAGTGCTAATGATATATAGCAATACACTA	600
622	CTCGTTACTGAGGCTACCAATCTACCGGAAGTGCTAATGATATATAGCAATACACTA	681
601	ATTAAACGGTAACCTCTCTCAACTATTAGTAATGACGAGGCAATCACTTTGGATAAA	660
682	ATTAAACGGTAACCTCTCTCAACTATTAGTAATGACGAGGCAATCACTTTAGATAAA	741
661	AAT 663	
742	AAT 744	

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RESULT 11
US-09-390-234-23
; Sequence 23, Application US/09390234
; Patent No. 6365390
; GENERAL INFORMATION:
; APPLICANT: Blum, David L.
; APPLICANT: Kataeva, Irina
; APPLICANT: Li, Xin-Liang
; APPLICANT: Ljungdahl, Lars G.
; TITLE OF INVENTION: Phenolic Acid Esterases, Coding Sequences and Methods
; FILE REFERENCE: 67-98
; CURRENT APPLICATION NUMBER: US/09/390,234
; CURRENT FILING DATE: 1998-09-03
; EARLIER APPLICATION NUMBER: US 60/099,136
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 2364
; TYPE: DNA
; ORGANISM: Clostridium stercoarium
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (440) ..(1975)
US-09-390-234-23

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	Query Match	38.5%	Score 255.4	DB 3	Length 2364	
	Best Local Similarity	65.6%	Pred. No. 7.9e-70			
	Matches 405	Conservative	0	Mismatches 206	Indels 6	Gaps 2
Qy	1	CAATCGTCACGCACAATTC	CAATGGCGAACACAGATGGCTATGATTCATGATATTTGGAAA	60		
Db	533	CGAATAATTTACGACATGAGACAGGACACATGGAGGCTACACATATGAGCTCTGGAAA	592			
Qy	61	GATAGCGGTGGCTCTGGGACAAATGATTC	CAATCATGGCGGTAACGTTCTAGTGCCCAATGG	120		
Db	593	GA---CTACGGAATACGATTTATGGAAC	TTAAACGACGCGTGTACTTTTAGTTGTCTCAATGG	649		
Qy	121	AACAATGTTAACACATATTTATTCGTTAAAGGTAAAAAATTC	CAATGAAACACAAAAACACAC	180		
Db	650	AGTAATATCGGTAATGCACTATTTAGAAAAGGGAGAAAATTTAAT	TTCGCGAANAACCTAT	709		

361	QY	ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGGATTGCCACA	420
439	Db	ACATATGATATCTATGAACTCTTAGAGTCAATCAGCCCTCCATTAAAGGGGATTGCCACA	498
421	QY	TTTAAACAAATATTGGAGTGTTTCGAAGATCGAAACGACGAGTGGCGACGATTTCTGTCCAGC	480
499	Db	TTTAAACAAATATTGGAGTGTCGGAAGATCGAAACGACGAGTGGCGACAAATTTCTGTCCAGC	558
481	QY	AACCACTTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGAAAAATCTATGAAAGTCGCG	540
559	Db	AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGAAAAATCTATGAAAGTCGCG	618
541	QY	CTTACTCTAGAGGCTATCAAAGTAGCGGAAGTGCTATGTATATAGCAATACACTAAGA	600
619	Db	CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTATGTATATAGCAATACACTAAGA	678
601	QY	ATTAACGGTAAACCTCTCTCAACTATTAGTATGACGAGAGCATAACTTCGATAAAAAC	660
679	Db	ATTAACGGAAAAACCTCTCTCAACTATTAGTATGACGAGAGCATAACTCTAGATAAAAAC	738
661	QY	AAAT 663	
739	Db	AAAT 741	
RESULT 10			
US-09-189-060B-11			
: Sequence 11, Application US/09189060B			

```

; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Dideriksen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Hybrid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(744)
; US-09-189-060B-11

Query Match          76.6%;      Score 507.8;  DB 3;      Length 744;
Best Local Similarity 85.4%;      Pred. No. 3.6e-149;
Matches 566; Conservative 0; Mismatches 97; Indels 0; Gaps 0

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82	CAAAATCGTCACCGACAAATTCATTGGCAACACCATGGCTATGATTATGAATTTTGGAAA	141
Db		
61	GATAGCGGTGGCTCTGGGACAAATGATTTCTCAATCATCGCGGTACGTTCAGTGCCCAATGG	120
Qy		
142	GATAGCGGTGGCTCTGGGACAAATGATTTCTCAATCATCGCGGTACGTTCAGTGCCCAATGG	201
Db		
121	AACAAATGTTAAACAACATATTTTCGGTAAAGTAAAAAATTCATGAAACACAAAAACAC	180
Qy		
202	AACAAATGTTAAACAACATATTTTCGGTAAAGTAAAAAATTCATGAAACACAAAAACAC	261
Db		
181	CAACAAAGTTGGTAAACATGTCCTATAAACTACGGAGCCAACTTCCAAACCAATGTTAATGGC	240
Qy		
262	CAACAAAGTTGGTAAACATGTCCTATAAACTATGGCGCAAACTTCAGCGCAAAACGGAAATGGC	321
Db		
343	CAACAAAGTTGGTAAACATGTCCTATAAACTATGGCGCAAACTTCAGCGCAAAACGGAAATGGC	300
Qy		

QY 181 CAACAAAGTTGTTAACTGTCATTAACACTACGAGGCAACTTCCACCAAAATGGTAATGG 240
DB 710 CAAGAATTTAGGAGACATAGTAGTTGAATATGGCTGTGATTACAATCCAAACGAAATTTCC 769
QY 241 TATTATATGCTGTATGTTGGAGTGTGACCTCTTGTGCAATATATTATTTGTCGACAGT 300
DB 770 TATTATGTTTACGGTTGGACAGAAATCCACTGGTTGAATATTTACATTTGTAGAAAGC 829
QY 301 TGGGGCAACTGGCGTCCACGAGGCAACGCTAAAGGGGACCATCAC---TGTGATGA 357
DB 830 TGGGGCAGCTGGCGTCCACTGGAGCAACACCCAAAGGAACCATCACACAGTGGATGGCA 889
QY 358 GGAACATATGATATACAGAGCTCTTAGAGTCAATCAACCTTCCATTAAGGGGATGGC 417
DB 890 GGTACTTATGAATATATGAAATCTACCGGTTAAATCGACCTTCCATCGATGAACTGG 949
QY 418 ACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCACGATTTCTGTC 477
DB 950 ACATTTCAACAATATTGGAGTGTTCGTACATCCNAGAGAAACGAGGAAACATATCTGTC 1009
QY 478 AGCAACCACTTTAGAGCGTGGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTTC 537
DB 1010 ACTGAACATTTTAAACAGTGGGAAAGATGGGCATCGGAATGGTAAAGATGTATGAAGTT 1069
QY 538 GCGCTTACTGTAGAGGCTCAAGTAGCGGAGTGTCTAATGTATATAGCAATACACTA 597
DB 1070 GCTCTTACCGTTGAAGTTTACAGAGCAGTGGGTACGCTAATGTATACAGAAATGAAATC 1129
QY 598 AGAATTAACGGTAACCC 614
DB 1130 AGAATAGGTGCAAAATCC 1146

RESULT 12

US-09-603-311-23
; Sequence 23, Application US/09603311
; Patent No. 6602700
; GENERAL INFORMATION:
; APPLICANT: Li, Xin-Liang
; APPLICANT: Ljungdahl, Lars G.
; APPLICANT: Azain, Michael J.
; APPLICANT: Davies, Edward T.
; APPLICANT: Shah, Ashit K.
; APPLICANT: Blum, David L.
; APPLICANT: Kataeva, Irina
; TITLE OF INVENTION: Phenolic Acid Esterases, Coding Sequences and Methods
; FILE REFERENCE: 67-98A
; CURRENT APPLICATION NUMBER: US/09/603,311
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/099,136
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/390,324
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 2364
; TYPE: DNA
; ORGANISM: Clostridium stercorarium
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (440)..(1975)
US-09-603-311-23

Query Match 38.5%; Score 255.4; DB 4; Length 2364;
Best Local Similarity 65.6%; Pred. No. 7.9e-70;
Matches 405; Conservative 0; Mismatches 206; Indels 6; Gaps 2;
QY 1 CAAATCGTACCGACAAATTCATTTGGCAACCAACGATGGCTATGATTAATGAAATTTGGAAA 60
DB 533 CGAATTAATTACGACAAATGAGACAGGCAACACATGGAGGCTACGACTATGAGTCTGGA 592

QY 61 GATACGGTGGCTCTGGGACAAATGATCTCAATCATGCGGTAGCTTCAGTGCCTCAATGG 120
DB 593 GA---CTACGGAATACGATTATGGAACCTTAACGACGGTGGTACTTTTAGTTGTCAAATGG 649
QY 121 AACAAATGTAACAATATTTATTCGTTAAAGTAAATAATTTCAATGAACACACAAACACAC 180
DB 650 AGTAATATCGGTAAATGCACTATTTAGAAAAGGGAGAAAATTTAAATTCGACAAAACCTTAT 709
QY 181 CAACAAGTTGGTAACATGTCATTAACACTACGAGGCAACCTTCCAAACCAAAATGGTAATGG 240
DB 710 CAAGAATTTAGGAGACATAGTAGTTGAATATGGCTGTGATTACAATCCAAACGAAATTTCC 769
QY 241 TATTATATGCTGTATGTTGGAGTGTTCGACCTCTTGTGCAATATATTATTTGTCGACAGT 300
DB 770 TATTATGTTTACGGTTGGACAGAAATCCACTGGTTGAATATTTACATTTGTAGAAAGC 829
QY 301 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGGACCATCAC---TGTGATGA 357
DB 830 TGGGGCAGCTGGCGTCCACTGGAGCAACACCCAAAGGAACCATCACACAGTGGATGGCA 889
QY 358 GGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTTCCATTAAGGGGATGGC 417
DB 890 GGTACTTATGAATATATGAAATCTACCGGTTAAATCGACCTTCCATCGATGAACTGG 949
QY 418 ACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCACGATTTCTGTC 477
DB 950 ACATTTCAACAATATTGGAGTGTTCGTACATCCAAAGAGAAACGAGGAAACATATCTGTC 1009
QY 478 AGCAACCACTTTAGAGCGTGGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTTC 537
DB 1010 ACTGAACATTTTAAACAGTGGGAAAGATGGGCATCGGAATGGTAAAGATGTATGAAGTT 1069
QY 538 GCGCTTACTGTAGAGGCTCAAGTAGCGGAGTGTCTAATGTATATAGCAATACACTA 597
DB 1070 GCTCTTACCGTTGAAGTTTACAGAGCAGTGGGTACGCTAATGTATACAGAAATGAAATC 1129
QY 598 AGAATTAACGGTAACCC 614
DB 1130 AGAATAGGTGCAAAATCC 1146

RESULT 13

US-08-275-526C-1
; Sequence 1, Application US/08275526C
; Patent No. 6180382
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: LAHAYE, ANDR E
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE
; APPLICANT: DETROZ, REN
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,526C
; FILING DATE: 15-JUL-1994

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE: Bacillus pumilus
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
; US-08-275-526C-1

Query Match      38.5%; Score 255.2; DB 3; Length 1022;
Best Local Similarity 65.5%; Pred. No. 5.9e-70;
Matches 406; Conservative 0; Mismatches 208; Indels 6; Gaps 2;

QY 13 GACAAATCCATTGGCAACACAGATGGCTATGATTATGAATTTTGGAAAGATAGCGGTGGC 72
DB 279 GATAATAGGATAGGACACACAGCGGATACGATTTTGAATTTATGGAAGGATTAC---GGA 335

QY 73 TCTGGGACAAATGATCTCAATCATGCGGTACGTTTCAGTCCCAATGGAACAATGTTTAAAC 132
DB 336 AATACCTCGATGACACCAATACCGCGGGGCACTTTAGTGCAGCTGGAACAATTTTGA 395

QY 133 AACATATTATTCGTAAGGTAAATAATTCATGAAACACAAACACCAACCAAGTTGGT 192
DB 396 AATGCTTTATTTCCAAAGGAAAGAGTTCGATTCCTAACTAACTCATCACTTGGC 455

QY 193 AACATGTCATTAACCTACGGAGCCAACTTCACCAACCAATGTTATGTTATGTC 252
DB 456 AACATCTCCATCAACCTACACAGCGACCTTTAAACCGCGGGGAAATTCCTATTTATGTC 515

QY 253 TATGTTGGACTGTTGACCTCTTGTGCAATATTATATTGTCAGACTTGGGCAACTGG 312
DB 516 TATGGCTGACAACTCTCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 575

QY 456 AACATCTCCATCAACCTACACAGCGACCTTTAAACCGCGGGGAAATTCCTATTTATGTC 515
DB 575 TATGGCTGACAACTCTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 632

QY 313 CGTCCACAGGACAGCCTAAGGAGCCATCATCTGTTGATGGAGGACATATGATATC 372
DB 576 CGTCCACAGG---AACGTATAAAGGATCATTTTATGCGATGGAGGACATATGACATA 632

QY 373 TAGGAGACTTTAGAGTCAATCAACCTCATTAAGGGGATTCACACATTTTAAACAATAT 432
DB 633 TATGAAACGCTCGGTGTCATGACCTCTTATCATTTGGAGAGCTTACCTTCACAAATAT 692

QY 433 TGGAGTGTTCGAGATCGAAACGACAGTGGCAGCAATTTCTGTCAGCAACCACTTTAGA 492
DB 693 TGGAGTGTAGCTCAACAAACAAACGACAAAGCGGAAACGCTCTCGTCACTGAGCATTTAAA 752

QY 493 GCGTGGGAAACCTTAGGATGAATATGGGAAATGATGAAGTCGCGCTTACTGTAGAA 552
DB 753 AAATGGGAAAGCTTAGCGATGCCAATGGGAAATGATGAACAGCATTAATCTGTAGAA 812

QY 553 GGCTATCAAAAGTACGGAAGTGTCTAATGTATATAGCAATACACTAAGAAATTAACGGTAA 612
DB 813 GGCTACGGAAGCAACGGAAGTGGATGTCATGACGAATCAGCTGATGATTCGATAAAG 872

QY 613 CCTCTCTCAACTATTAGTAA 632
DB 873 CATATGAAAGGAGCAGCAA 892

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RESULT 14
US-08-275-526C-35
; Sequence 35, Application US/08275526C

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; Patent No. 6180382
; GENERAL INFORMATION:
; APPLICANT: DE BOYL, ERIC
; APPLICANT: LAHAYE, ANDR E
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE
; APPLICANT: DETROZ, REN
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,526C
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-08-275-526C-35

Query Match      38.5%; Score 255.2; DB 3; Length 1022;
Best Local Similarity 65.5%; Pred. No. 5.9e-70;
Matches 406; Conservative 0; Mismatches 208; Indels 6; Gaps 2;

QY 13 GACAAATCCATTGGCAACACAGATGGCTATGATTATGAATTTTGGAAAGATAGCGGTGGC 72
DB 279 GATAATAGGATAGGACACACAGCGGATACGATTTTGAATTTATGGAAGGATTAC---GGA 335

QY 73 TCTGGGACAAATGATCTCAATCATGCGGTACGTTTCAGTCCCAATGGAACAATGTTTAAAC 132
DB 336 AATACCTCGATGACACCAATACCGCGGGGCACTTTAGTGCAGCTGGAACAATTTTGA 395

QY 133 AACATATTATTCGTAAGGTAAATAATTCATGAAACACAAACACCAACCAAGTTGGT 192
DB 396 AATGCTTTATTTCCAAAGGAAAGAGTTCGATTCCTAACTAACTCATCACTTGGC 455

QY 193 AACATGTCATTAACCTACGGAGCCAACTTCACCAACCAATGTTATGTTATGTC 252
DB 456 AACATCTCCATCAACCTACACAGCGACCTTTAAACCGCGGGGAAATTCCTATTTATGTC 515

QY 253 TATGTTGGACTGTTGACCTCTTGTGCAATATTATATTGTCAGACTTGGGCAACTGG 312
DB 516 TATGGCTGACAACTCTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 575

QY 456 AACATCTCCATCAACCTACACAGCGACCTTTAAACCGCGGGGAAATTCCTATTTATGTC 515
DB 575 TATGGCTGACAACTCTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 632

QY 313 CGTCCACAGGACAGCCTAAGGAGCCATCATCTGTTGATGGAGGACATATGATATC 372
DB 576 CGTCCACAGG---AACGTATAAAGGATCATTTTATGCGATGGAGGACATATGACATA 632

QY 373 TAGGAGACTTTAGAGTCAATCAACCTCATTAAGGGGATTCACACATTTTAAACAATAT 432
DB 633 TATGAAACGCTCGGTGTCATGACCTCTTATCATTTGGAGAGCTTACCTTCACAAATAT 692

QY 433 TGGAGTGTTCGAGATCGAAACGACAGTGGCAGCAATTTCTGTCAGCAACCACTTTAGA 492
DB 693 TGGAGTGTAGCTCAACAAACAAACGACAAAGCGGAAACGCTCTCGTCACTGAGCATTTAAA 752

QY 493 GCGTGGGAAACCTTAGGATGAATATGGGAAATGATGAAGTCGCGCTTACTGTAGAA 552
DB 753 AAATGGGAAAGCTTAGCGATGCCAATGGGAAATGATGAACAGCATTAATCTGTAGAA 812

QY 553 GGCTATCAAAAGTACGGAAGTGTCTAATGTATATAGCAATACACTAAGAAATTAACGGTAA 612
DB 813 GGCTACGGAAGCAACGGAAGTGGATGTCATGACGAATCAGCTGATGATTCGATAAAG 872

QY 613 CCTCTCTCAACTATTAGTAA 632
DB 873 CATATGAAAGGAGCAGCAA 892

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Db 576 CGTCCACAGG--AACGTATTAAGGATCATTTTATCCGATGGAGGCACATATGACATA 632
Qy 373 TAGGAGACTCTTAGAGTCAATCAACCTCCATTAGGGGATTCGCCACATTTAAACAATAT 432
Db 633 TATGAACCGCTCGGTGTCATCAGCCTTCTATCATTTGGAGAGCGCTACCTTCAACAATAT 692
Qy 433 TGGAGTGTTCGAAGATCGAAACGCGAGGTGGCAGGATTTCTGTCAAGCAACCACTTTAGA 492
Db 693 TGGAGTGTACGTCAAAACAAACGCAACGCGAAGCGTCTCGTCAAGTACGATTTTAA 752
Qy 493 GCGTGGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTCCGCTTACTGTAGAA 552
Db 753 AAATGGGAAGCTTAGCGATGCCAATGGGAAATGTATGAACACAGCATTAACGTAGAA 812
Qy 553 GGCTATCAAGTAGCGGAGTGTATATGTATATAGCAATACACTAAGAAATTAACGGTAA 612
Db 813 GGCTACCGAAGCAACGGAAGTGGGAATGTATGACGAATCAGCTGATGATTCGATAAAG 872
Qy 613 CCTCTCTCAACTATTAGTAA 632
Db 873 CATATGAAAAGCCAGCAA 892

RESULT 15

US-09-076-677-1
Sequence 1, Application US/09076677

Patent No. 6423523

GENERAL INFORMATION:

APPLICANT: DE BUYL, ERIC

LAHAYE, ANDREE

LEDOUX, PIERRE

AMORY, ANTOINE

DETROZ, RENE

ANDRE, CHRISTOPHE

VETTER, ROMAN

TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSON VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P. C.

STREET: 2000 K St., N.W., Suite 200

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/076.677

FILING DATE: 12-May-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/275,526

FILING DATE: 15-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Gadiano, Wilhem P.

REGISTRATION NUMBER: 37,136

REFERENCE/DOCKET NUMBER: 4121-49

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 429-0625

TELEFAX: (202) 293-0625

TELEX: 650 383 5605

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1022 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus pumilus
STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-076-677-1

Query Match 38.5%; Score 255.2; DB 4; Length 1022;
Best Local Similarity 65.5%; Pred. No. 5.9e-70;
Matches 406; Conservative 0; Mismatches 208; Indels 6; Gaps 2;

Qy 13 GACAAATTCATTGGCAACACGATGGCTATGATTAATTTTGAAGATAGCGGTGC 72
Db 279 GATAATAGGATAGGACACACAGCGGATACGATTTTGAATTTATGAAGGATTAC---GGA 335
Qy 73 TCTGGGCAATCAATCTCAATCATGCGGTAGTTCAGTGCCTCAATGGAACCAATGTAAC 132
Db 336 AATACCTCGATGACACTCAATTAACGCGGGGCGCATTTAGTGGCAAGCTGGAAACAATATGGA 395
Qy 133 AACATATTATTCGTAAGGTAAAAAATTTCAATGAACACAAACACACCAACCAAGTTGGT 192
Db 396 AATGCTTTATTTGAAAAGGAAGAGTTTGTATCCACTAAAACTCATCATCACTTGGC 455
Qy 193 AACATGTCCATAAACTACGGAGCCCACTTCCAAACCAATGGTAATGCGTATTTATCGCTC 252
Db 456 AACATCTCCATCAACTACAAACGAGCCTTTAAACCGGGCGGAAATTCCTATTTATGTGC 515
Qy 253 TATGGTTGGACTGTTGACCCCTCTTGTGCAATATATTTATGTCGACAGTTGGGCAACTGG 312
Db 516 TATGGCTGGACACAATCTCCATTAGCTGAATACTACATTTGTTGAGTCATGGGGCACAAT 575
Qy 313 CGTCACACGAGGAGCAACGCTAAGGGGACCATCTGTTGATGGAGGAACATATGATATC 372
Db 576 CGTCCACAGG---AACGTATTAAGGATCATTTTATGCCGATGGAGGCACATATGACATA 632
Qy 373 TAGGAGACTCTTAGAGTCAATCAACCTCCATTAGGGGATTCGCCACATTTAAACAATAT 432
Db 633 TATGAACCGCTCGGTGTCATCAGCCTTCTATCATTTGGAGAGCGCTACCTTTCAACAATAT 692
Qy 433 TGGAGTGTTCGAAGATCGAAACGCGAGTGGCAGCATTTCTGTCAAGCAACCACTTTAGA 492
Db 693 TGGAGTGTACGTCAAAACAAACGCAACGGAACCGTCTCCGTCAAGTACGATTTTAA 752
Qy 493 GCGTGGGAAAACTTAGGGATGAATATGGGAAAAATGTATGAAGTCGCGCTTACTGTAGAA 552
Db 753 AAATGGGAAAGCTTAGGCATGCCAATGGGAAAAATGTATGAACACAGCATTTAAGTAA 812
Qy 553 GGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGAAATTAACGGTAA 612
Db 813 GGCTACCGAAGCAACGGAAGTGGCAATGTATGACGAATCAGTCAAGCAATCAGTATCGATAAAG 872
Qy 613 CCTCTCTCAACTATTAGTAA 632
Db 873 CATATGAAAAGCCAGCAA 892

Search completed: November 11, 2004, 01:34:19
Job time : 79.1638 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 10, 2004, 15:55:17 ; Search time 420.566 Seconds
(without alignments)
8275.436 Million cell updates/sec

Title: US-09-909-207-1
Perfect score: 663
Sequence: 1 CAATCGTCACGACAATTC.....TAACCTTTCGATATAAACAAAT 663

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001bs: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	663	2	AAT16101 Xylanase
2	663	100.0	744	2	AAT16102 Xylanase
3	663	100.0	1513	2	AAT16103 Xylanase
4	634.2	95.7	744	2	AAT13067 Glycoyl
5	634.2	95.7	871	2	AAT30255 DNA encod
6	624.6	94.2	744	2	AAT92878 Thermosta
7	607.8	76.6	747	2	AAT13074 Xylanase
8	371.2	56.0	1068	12	ADJ34947 DNA encod
9	276.4	41.7	1956	12	ADJ35051 DNA encod
10	255.4	38.5	2364	3	AAT21821 Clostridi
11	255.2	38.5	1022	2	AAT90923 B. pumilu
12	255	38.5	684	12	ADJ34969 DNA encod
13	212.2	32.0	1190	2	AAT90972 Nucleotid
14	204.8	30.9	1244	2	AAT08142 Xylanase
15	177.8	26.8	747	12	ADJ35011 DNA encod
16	154.4	23.3	164	2	AAT92876 Thermosta
17	151.2	22.8	164	2	AAT92875 Thermosta
18	143.6	21.7	1695	12	ADJ35101 DNA encod
19	141.2	21.3	1338	12	ADJ35151 DNA encod
20	136.2	20.5	1077	12	ADJ34965 DNA encod
21	130.2	19.6	1065	12	ADJ34999 DNA encod

22	128.4	19.4	1047	12	ADJ34949	Adj34949 DNA encod
23	121.2	18.3	678	12	ADJ34955	Adj34955 DNA encod
24	119.4	18.0	1375	2	AAX90405	Aax90405 Actinomad
25	119.4	18.0	1375	2	AAT64930	Aat64930 Actinomad
26	119	17.9	229	2	AAV15063	Aav15063 Xylanase
27	118.4	17.9	573	2	AAV36098	Aav36098 DNA seque
28	117.8	17.8	1207	2	AAT42374	Aat42374 Bacillus
29	117.6	17.7	1041	12	ADJ34943	Adj34943 DNA encod
30	116.8	17.6	1047	12	ADJ35083	Adj35083 DNA encod
31	115.2	17.4	213	2	AAV15059	Aav15059 Xylanase
32	115.2	17.4	596	3	AAA48219	Aaa48219 T. reesei
33	115.2	17.4	596	6	AAD29410	Aad29410 Trichoder
34	115.2	17.4	596	9	AAL60925	Aal60925 Trichoder
35	115.2	17.4	596	9	AAL60941	Aal60941 Trichoder
36	112	16.9	1074	12	ADJ34983	Adj34983 DNA encod
37	112	16.9	1137	12	ADJ35039	Adj35039 DNA encod
38	111.8	16.9	1273	2	AAQ90388	Aaq90388 Xylanase
39	111.4	16.8	636	12	ADJ34981	Adj34981 DNA encod
40	111.4	16.8	942	10	ABQ80366	Abq80366 A. fumiga
41	111.2	16.8	1008	12	ADJ35015	Adj35015 DNA encod
42	110.8	16.7	669	12	ADJ34951	Adj34951 DNA encod
43	110.4	16.7	1047	12	ADJ35037	Adj35037 DNA encod
44	110	16.6	1002	10	ABQ80365	Abq80365 A. fumiga
45	109.4	16.5	1041	12	ADJ34953	Adj34953 DNA encod

ALIGNMENTS

RESULT 1
AAT16101
ID AAT16101 standard; DNA; 663 BP.
XX AC AAT16101;
XX 16-OCT-2003 (revised)
DT 15-MAY-1996 (first entry)
XX Xylanase gene.
XX Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
KW ss.
XX Bacillus sp; strain 710/1 (LMG P-14798):
XX Key Location/Qualifiers
FT mat_peptide 1..663
FT /tag= a
FT /EC_number= "3.2.1.8"
XX
XX AU9525086-A.
XX 08-FEB-1996.
XX 19-JUL-1995; 95AU-00025086.
XX 26-JUL-1994; 94BE-00000706.
XX 17-MAY-1995; 95BE-00000448.
XX (SOLV) SOLVAY SA.
XX De Buyl E, Lahaye A, Ledoux P, Detroz R;
XX WPI; 1996-117341/13.
XX P-PSDB; AAR92053.
XX Bacillus derived xylanase active over wide pH range - used in treatment
XX of paper pulp, animal feeds and in bakery goods.
XX Claim 30; Page 50-51; 94pp; English.
XX A DNA sequence (AAT16101) coding for a thermostable mature xylanase
XX (AAR92053) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-
CC

Applicant's
work
priority claimed

CC 14798). Sequences were also obtd. (see AAT16102 and AAT16103) for the
CC xylanase precursor and for the complete gene including 5' and 3',
CC untranslated sequences. DNA coding for the mature enzyme may be
CC incorporated into a vector and expressed from either its own promoter or
CC from the Bacillus pumilus PRL B12 promoter (AAQ73996), and used for
CC prodn. of recombinant xylanase in transformed hosts, pref. Bacillus
CC licheniformis or B. pumilus. The enzyme is useful in the paper-pulp,
CC animal feed and baking industries. (Updated on 16-OCT-2003 to standardise
CC OS field)

XX SQ Sequence 663 BP; 220 A; 131 C; 146 G; 166 T; 0 U; 0 Other;

Query Match 100.0%; Score 663; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 5e-188;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATCGTCACGCAATTCATGGCAACACGATGGCTATGATTAATTTGGAAA 60
DB 1 CAATCGTCACGCAATTCATGGCAACACGATGGCTATGATTAATTTGGAAA 60
QY 61 GATACGGTGGCTCTGGGACATGATTCCTCAATCATGGCGGTACGTTCCAGTCCCAATGG 120
DB 61 GATACGGTGGCTCTGGGACATGATTCCTCAATCATGGCGGTACGTTCCAGTCCCAATGG 120
QY 121 AACAAATGTTAAACAATATTTTCGGTAAAGGTAAAAAATTCATGAAACAACAACACAC 180
DB 121 AACAAATGTTAAACAATATTTTCGGTAAAGGTAAAAAATTCATGAAACAACAACACAC 180
QY 181 CAACAAGTGGTAAACATGTCCTCAATACGAGGCACTTCCACCAAAATGGTAATGCG 240
DB 181 CAACAAGTGGTAAACATGTCCTCAATACGAGGCACTTCCACCAAAATGGTAATGCG 240
QY 241 TATTATGCGTCTATGGTGGACTGTGACCCCTCTGTGCGAATATTAATTTGCGACAGT 300
DB 241 TATTATGCGTCTATGGTGGACTGTGACCCCTCTGTGCGAATATTAATTTGCGACAGT 300
QY 301 TGGGCAACTGGCTCCACGAGCAACGCTTAAGGGGACCATCAGTGTGATGGAGA 360
DB 301 TGGGCAACTGGCTCCACGAGCAACGCTTAAGGGGACCATCAGTGTGATGGAGA 360
QY 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGCCACA 420
DB 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGCCACA 420
QY 421 TTTAAACAATATGGAGTGTTCGAGATCGAAACGACGAGTGGCAGCTTCTGTGAGC 480
DB 421 TTTAAACAATATGGAGTGTTCGAGATCGAAACGACGAGTGGCAGCTTCTGTGAGC 480
QY 481 AACCACTTTAGACGCTGGGAAACTTAGGATGAATATGGGAAATATGATGAGTTCGCG 540
DB 481 AACCACTTTAGACGCTGGGAAACTTAGGATGAATATGGGAAATATGATGAGTTCGCG 540
QY 541 CTTACTGTAGAGGCTATCAAGTACGGAAGTCTTAATGTATATAGCAATACATAAGA 600
DB 541 CTTACTGTAGAGGCTATCAAGTACGGAAGTCTTAATGTATATAGCAATACATAAGA 600
QY 601 ATTAAGGTTAACCCCTCTCAACTATAGTATGACGAGCATACCTTTGATATAAAC 660
DB 601 ATTAAGGTTAACCCCTCTCAACTATAGTATGACGAGCATACCTTTGATATAAAC 660
QY 661 AAT 663
DB 661 AAT 663

RESULT 2
ID AAT16102
XX AAT16102 standard; DNA; 744 BP.
AC AAT16102;
XX
XX 16-OCT-2003 (revised)
DT 15-MAY-1996 (first entry)
DT

XX Xylanase precursor gene.
DE Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
KW ss.
KW Bacillus sp; strain 710/1 (LMG P-14798).
OS

XX Key Location/Qualifiers
FH sig_peptide 1..81 /tag= a
FT mat_peptide 82..744 /tag= b
FT /EC_number= "3.2.1.8"

XX AU9525086-A.
XX 08-FEB-1996.
XX 19-JUL-1995; 95AU-00025086.
XX 26-JUL-1994; 94BE-00000706.
XX 17-MAY-1995; 95BE-00000448.
XX (SOLV) SOLVAY SA.

XX De Buyl E, Lahaye A, Ledoux P, Detroz R;
XX WPI; 1996-117341/13.
XX P-PSDB; AAR92054.

XX Bacillus derived xylanase active over wide pH range - used in treatment
XX of paper pulp, animal feeds and in bakery goods.
XX Claim 9; Page 54-55; 94pp; English.

XX A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was
XX isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The
XX sequence (AAT16103) for the complete gene including 5' and 3',
XX untranslated sequences was also obtd. The gene may be incorporated into a
XX vector and expressed from either its own promoter or from the Bacillus
XX pumilus PRL B12 promoter (see AAQ73996), and used for prodn. of
XX recombinant thermostable xylanase in transformed hosts, pref. Bacillus
XX licheniformis or B. pumilus. The enzyme is useful in the paper-pulp,
XX animal feed and baking industries. (Updated on 16-OCT-2003 to standardise
XX OS field)

XX SQ Sequence 744 BP; 246 A; 144 C; 160 G; 194 T; 0 U; 0 Other;

Query Match 100.0%; Score 663; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 5.3e-188;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATCGTCACGCAATTCATGGCAACACGATGGCTATGATTAATTTGGAAA 60
DB 82 CAATCGTCACGCAATTCATGGCAACACGATGGCTATGATTAATTTGGAAA 141
QY 61 GATACGGTGGCTCTGGGACATGATTCCTCAATCATGGCGGTACGTTCCAGTCCCAATGG 120
DB 142 GATACGGTGGCTCTGGGACATGATTCCTCAATCATGGCGGTACGTTCCAGTCCCAATGG 201
QY 121 AACAAATGTTAAACAATATTTTCGGTAAAGGTAAAAAATTCATGAAACAACAACACAC 180
DB 202 AACAAATGTTAAACAATATTTTCGGTAAAGGTAAAAAATTCATGAAACAACAACACAC 261
QY 181 CAACAAGTGGTAAACATGTCCTCAATACGAGGCACTTCCACCAAAATGGTAATGCG 240.
DB 262 CAACAAGTGGTAAACATGTCCTCAATACGAGGCACTTCCACCAAAATGGTAATGCG 321
QY 241 TATTATGCGTCTATGGTGGACTGTGACCCCTCTGTGCGAATATTAATTTGCGACAGT 300
DB 322 TATTATGCGTCTATGGTGGACTGTGACCCCTCTGTGCGAATATTAATTTGCGACAGT 381

QY 301 TGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCATCAGTGTGGTGGAGGA 360
 DB |||||
 QY 382 TGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCATCAGTGTGGTGGAGGA 441
 DB |||||
 QY 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGGATTGCCACA 420
 DB |||||
 QY 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGGATTGCCACA 501
 DB |||||
 QY 421 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGGACCAATTTCTGTGAGC 480
 DB |||||
 QY 502 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGGACCAATTTCTGTGAGC 561
 DB |||||
 QY 481 RACCACTTTAGAGCGTGGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTCCGG 540
 DB |||||
 QY 562 RACCACTTTAGAGCGTGGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTCCGG 621
 DB |||||
 QY 541 CTTACTGTAGAGGCTATCAAAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 600
 DB |||||
 QY 622 CTTACTGTAGAGGCTATCAAAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 681
 DB |||||
 QY 601 ATTAACGGTAACCCCTCTCTCAACTATTAGTAAATGACGAGAGCATAACTTTGGATAAAAC 660
 DB |||||
 QY 682 ATTAACGGTAACCCCTCTCTCAACTATTAGTAAATGACGAGCATAACTTTGGATAAAAC 741
 DB |||||
 QY 661 AAT 663
 DB 742 AAT 744

RESULT 3
 ID AAT16103 standard; DNA; 1513 BP.

XX AAT16103;

DT 16-OCT-2003 (revised)
 DT 15-MAY-1996 (first entry)

XX Xylanase gene.

DE Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
 KW 86.

XX Bacillus sp; strain 710/1 (LMG P-14798).

XX Key Location/Qualifiers
 FT promoter 1. .619

FT CDS /*tag= a
 620..1366

FT sig_peptide /*tag= b
 620..600

FT mat_peptide /*tag= c
 701..1363

FT /*tag= d
 /BC number= "3.2.1.8"

FT 3'UTR 1367..1513
 FT /*tag= e

XX AU9525086-A.

XX 08-FEB-1996.

XX 19-JUL-1995; 95AU-00025086.

XX 26-JUL-1994; 94BE-00000706.

XX 17-MAY-1995; 95BE-00000448.

XX (SOLV) SOLVAY SA.

XX De Buyl E, Lahaye A, Ledoux P, Detroz R;

XX WPI; 1996-117341/13.

XX P-PSDB; AAR92054.

XX Bacillus derived xylanase active over wide pH range - used in treatment
 PT of paper pulp, animal feeds and in bakery goods.
 XX Claim 10; Page 59-61; 94pp; English.
 XX A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was
 CC isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The
 CC gene may be incorporated into a vector and expressed in transformed
 CC hosts, pref. Bacillus licheniformis or Bacillus pumilus, for prodn. of
 CC thermostable mature xylanase (AAR92053). The enzyme is useful in the
 CC paper pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX Sequence 1513 BP; 500 A; 282 C; 271 G; 460 T; 0 U; 0 Other;

Query Match 100.0%; Score 663; DB 2; Length 1513;
 Best Local Similarity 100.0%; Pred. No. 7.1e-188;
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATCGTCACCGCAAAATTCATTTGGCAACCAACGATGGCTATGATTATCAATTTGGAAA 60
 DB 701 CAATCGTCACCGCAAAATTCATTTGGCAACCAACGATGGCTATGATTATCAATTTGGAAA 760
 QY 61 GATAGCGTGGCTCTGGGACAATGATTTCAATCAATGCGGTACGTTGAGTCCCAATGG 120
 DB 761 GATAGCGTGGCTCTGGGACAATGATTTCAATCAATGCGGTACGTTGAGTCCCAATGG 820
 QY 121 AACAAATGTTAACACATATTTTCGTTAAAGTAAATAATTCATTAAGTAAACACACACAC 180
 DB 821 AACAAATGTTAACACATATTTTCGTTAAAGTAAATAATTCATTAAGTAAACACACACAC 880
 QY 181 CAACAAGTTGGTAACATGTCATTAACCTACGAGGCAACCTCCAAACCAATGGTATGG 240
 DB 881 CAACAAGTTGGTAACATGTCATTAACCTACGAGGCAACCTCCAAACCAATGGTATGG 940
 QY 241 TATTATGCGTCTATGGTTGGACTGTTGACCCCTCTTGTGCAATATATATGTCAGACGT 300
 DB 941 TATTATGCGTCTATGGTTGGACTGTTGACCCCTCTTGTGCAATATATATGTCAGACGT 1000
 QY 301 TGGGGCAACTGGCGTCCACGAGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGA 360
 DB 1001 TGGGGCAACTGGCGTCCACGAGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGA 1060
 QY 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTGCCACA 420
 DB 1061 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTGCCACA 1120
 QY 421 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGGACCAATTTCTGTGAGC 480
 DB 1121 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGGACCAATTTCTGTGAGC 1180
 QY 481 AACCACTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGGGAAAATGTATGAAGTCCGG 540
 DB 1181 AACCACTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGGGAAAATGTATGAAGTCCGG 1240
 QY 541 CTTACTGTAGAGGCTATCAAAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 600
 DB 1241 CTTACTGTAGAGGCTATCAAAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 1300
 QY 601 ATTAACGGTAACCCCTCTCTCAACTATTAGTAAATGACGAGAGCATAACTTTGGATAAAAC 660
 DB 1301 ATTAACGGTAACCCCTCTCTCAACTATTAGTAAATGACGAGAGCATAACTTTGGATAAAAC 1360
 QY 661 AAT 663
 DB 1361 AAT 1363

RESULT 4
 AAV13067
 ID AAV13067 standard; DNA; 744 BP.
 XX

Appl. Work

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AC AAV13067;
XX
DT 19-MAY-1998 (first entry)
XX
DE Glycosyl hydrolase family 11 xylanase DNA derived from Bacillus sp.
XX
DE Glycosyl hydrolase family 11; isolation;
XX
KW Bacillus sp; xylanase; glycosyl hydrolase family 11;
XX
KW microorganism; identification; ss.
XX
OS Bacillus sp.
XX
PH Location/Qualifiers
FT CDS
FT 1..747
FT /tag= a
FT /product= "glycosyl hydrolase family 11 xylanase"
XX
XX
XX WO9743409-A2.
XX
XX 20-NOV-1997.
XX
XX 12-MAY-1997; 97WO-DK000216.
XX
XX 10-MAY-1996; 96DK-00000562.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Dalboge H, Diderichsen B, Sandal T, Kauppinen S;
XX
XX WPI; 1998-008878/01.
XX
XX P-PSDB; AAW44262.
XX
XX
XX Isolating novel DNA sequences from microorganisms - without the need for
XX
XX culturing the microorganism.
XX
XX Example 1; Page 31-32; 72pp; English.
XX
XX The present sequence encodes a polypeptide with xylanase activity used in
XX
XX an example of the present invention. The present invention describes a
XX
XX novel method for providing a novel DNA sequence encoding a polypeptide
XX
XX from a microorganism with an activity of interest. The method comprises:
XX
XX (i) PCR amplification of the DNA with PCR primers with homology to (a)
XX
XX known gene(s) encoding a polypeptide with an activity of interest; (ii)
XX
XX linking the obtained PCR product of a 5' structural gene sequence and a
XX
XX 3' structural gene sequence; (iii) expressing the resulting hybrid DNA
XX
XX sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide
XX
XX with the activity of interest or a related activity; and (v) isolating
XX
XX the hybrid DNA sequence identified in step (iv). This method provides for
XX
XX identification and isolation of sequences from microorganisms without
XX
XX having to cultivate and isolate the microorganism
XX
XX
XX Sequence 744 BP; 249 A; 146 C; 157 G; 192 T; 0 U; 0 Other;
XX
XX
XX Query Match 95.7%; Score 634.2; DB 2; Length 744;
XX
XX Best Local Similarity 97.3%; Pred. No. 2.2e-179;
XX
XX Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX
XX
XX 1 CAAATCGTCACGCAATTCATTGCGACACGATGGCTATGATTGAATTTGGAAA 60
XX
XX 82 CAAATCGTCACGCAATTCATTGCGACACGATGGCTATGATTGAATTTGGAAA 141
XX
XX
XX 61 GATAGCGGTGGCTCTGGGACATGATTTCTCAATCATGGCGGTACGTTCCAGTGCCCAATGG 120
XX
XX 142 GATAGCGGTGGCTCTGGGACATGATTTCTCAATCATGGCGGTACGTTCCAGTGCCCAATGG 201
XX
XX
XX 121 AACATGTTTAAACAATATTATTCGTTAAAGTAAATAATTCATGAACACACACAC 180
XX
XX 202 AACATGTTTAAACAATATTATTCGTTAAAGTAAATAATTCATGAACACACACAC 261
XX
XX
XX 181 CAACAAGTTGGTAAACATGTCCTAAATACGAGGACCACTTCCAAACCAATGGTAAATGG 240
XX
XX 262 CAACAAGTTGGTAAACATGTCCTAAATACGAGGACCACTTCCAAACCAATGGTAAATGG 321
XX
XX
XX 241 TATTTATGCGTCTATGGTTGGACTGTGTGACCTCTGTTCGAATATATATTTGTCGACAGT 300

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Db 322 TATTTATGCGTCTATGGTTGGACTGTGTGACCTCTGTTCGAATATATATTTGTCGATAGT 381
Qy 301 TGGGGCAACTGGCGTCCACCAGAGCAACGCTTAAGGGGACCACCTACTGTTGATGGAGGA 360
Db 382 TGGGGCAACTGGCGTCCACCAGGGGCAACGCTTAAGGGGACCACCTACTGTTGATGGAGGA 441
Qy 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAAGGGGATTCGCACA 420
Db 442 ACATATGATATCTATGAACTCTTAGAGTCAATCAGCCCTCCATTAAAGGGGATTCGCACA 501
Qy 421 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTGAGC 480
Db 502 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTGAGC 561
Qy 481 AACCACTTTAGAGCGTGGGAAACTTAGGATGATATGGGAAATCTATGAAAGTCGCG 540
Db 562 AACCACTTTAGAGCGTGGGAAACTTAGGATGATATGGGAAATCTATGAAAGTCGCG 621
Qy 541 CTTACTGTAGAAGGCTATCAAAGTAGCGGAGTCTAATGTATATAGCAATFACACTAAGA 600
Db 622 CTTACTGTAGAAGGCTATCAAAGTAGCGGAGTCTAATGTATATAGCAATFACACTAAGA 681
Qy 601 ATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAC 660
Db 682 ATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTAGATAAAAC 741
Qy 661 AAT 663
Db 742 AAT 744

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RESULT 5

AAV30255
ID AAV30255 standard; DNA; 871 BP.

XX AC AAV30255;
XX
XX 17-OCT-2003 (revised)
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 18-AUG-1998 (first entry)
XX
XX DNA encoding a Bacillus agaradherens xylanolytic enzyme.
XX
XX Xylanolytic enzyme; Bacillus agaradherens NCIMB 40482; breakdown;
XX agricultural waste; alcohol fuel; enzymatic treatment; animal feed;
XX release; free pentose sugar; dissolving pulp; cellulose; bio-bleaching;
XX wood pulp; lignocellulosic material; animal feed additive; ss.
XX
XX Bacillus agaradherens.

XX Key Location/Qualifiers
XX CDS 82..747
XX FT /tag= a

XX US5770424-A.

XX 23-JUN-1998.

XX 16-AUG-1996; 96US-00698978.

XX 02-JUL-1993; 93WO-DK000218.

XX 30-NOV-1994; 94US-00343600.

XX 06-JUN-1995; 95US-00470398.

XX (NOVO) NOVO-NORDISK AS.

XX Outtrup H, Bisgard-Frantzen H, Schuelein M, Olsen AA;

XX Jorgensen PL, Dambmann C;

XX WPI; 1998-376805/32.

XX P-PSDB; AAW60562.

XX DNA construct encoding *Bacillus agaradherens* xylanolytic enzyme - and
PT vectors and *Bacillus* cells containing these, useful for recombinant
PT production of the enzyme for use in agricultural waste breakdown and
PT lignocellulosic material treatment.
XX
PS Claim 1; Col 11-14; 10pp; English.
XX
XX The present sequence encodes a xylanolytic enzyme of *Bacillus*
CC *agaradherens* NCIMB 40482. Xylanolytic enzymes are used for enzymatic
CC breakdown of agricultural wastes for production of alcohol fuels,
CC enzymatic treatment of animal feeds to release free pentose sugars,
CC manufacturing of dissolving pulps yielding cellulose and bio-bleaching of
CC wood pulp. They are also used for treatment of lignocellulosic material
CC e.g. paper and pulp, or as an animal feed additive. (Updated on 25-MAR-
CC 2003 to correct PI field.) (Updated on 25-MAR-2003 to correct PI field.)
CC (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 871 BP; 283 A; 171 C; 179 G; 238 T; 0 U; 0 Other;

Query Match 95.7%; Score 634.2; DB 2; Length 871;
Best Local Similarity 97.3%; Pred. No. 2.4e-179;
Matches 645; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 CAAATCGTCACGCAAAATTCATTCGCAACGAGTGGCTATGATTAATTTGGAAA 60
DB 82 CAAATCGTCACGCAAAATTCATTCGCAACGAGTGGCTATGATTAATTTGGAAA 141
QY 61 GATAGCGGTGGCTCTCGGCAATGATTCATCATGCGGGTACGTTCAAGTCCCAATGG 120
DB 142 GATAGCGGTGGCTCTCGGCAATGATTCATCATGCGGGTACGTTCAAGTCCCAATGG 201
QY 121 AACAAATGTTAAACAATATTTTCGTAAGGTAAATAATTCATCAAAACACAAACACAC 180
DB 202 AACAAATGTTAAACAATATTTTCGTAAGGTAAATAATTCATCAAAACACAAACACAC 261
QY 181 CAAAGATGTTAAACAATGTTCAATACGAGGCAACCTTCCAAACCAATGTAATGCG 240
DB 262 CAAAGATGTTAAACAATGTTCAATACGAGGCAACCTTCCAAACCAATGTAATGCG 321
QY 241 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTAATTTGCGACAGT 300
DB 322 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTAATTTGCGACAGT 381
QY 301 TGGGGCAACTGGCGTCCACGAGCAACGCTTAAGGGGACCATCATCTGTTGATGAGGA 360
DB 382 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGGACCATCATCTGTTGATGAGGA 441
QY 361 ACATATGATATCTACGAGACTCTAGAGTCAATCAACCCCTCAATTAAGGGGATTCACCA 420
DB 442 ACATATGATATCTATGAATCTCTAGAGTCAATCAACCCCTCAATTAAGGGGATTCACCA 501
QY 421 TTTTAAACAATTTGGAGTGTTCGAAGATCAAAACGACGAGTGGCAGATTTCTGTGACG 480
DB 502 TTTTAAACAATTTGGAGTGTTCGAAGATCAAAACGACGAGTGGCAGATTTCTGTGACG 561
QY 481 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATGCGGAAAATGTAATGAAGTCGG 540
DB 562 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATGCGGAAAATGTAATGAAGTCGG 621
QY 541 CTTACTGTAGAGGCTATCAAGTAGCGGGAAGTGTCTATGATATAGCAATACACTAAGA 600
DB 622 CTTACTGTAGAGGCTATCAAGTAGCGGGAAGTGTCTATGATATAGCAATACACTAAGA 681
QY 601 ATTAACGGTAACCTCTCTCAACTATTAGTAAGACGAGAGCACTTAATTTGGGATAAAAC 660
DB 682 ATTAACGGTAACCTCTCTCAACTATTAGTAAGACGAGAGCACTTAATTTGGGATAAAAC 741
QY 661 AAT 663
DB 742 AAT 744

RESULT 6

AAQ92878
ID AAQ92878 standard; DNA; 744 BP.
XX
XX AAQ92878;
XX
XX 16-OCT-2003 (revised)
DT 12-PEB-1996 (first entry)
XX
XX Thermostable alkaline endo-1,4-beta-D-xylanase gene.
DE thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning;
KW polymerase chain reaction; *Escherichia coli*; EC-3.2.1.8; paper; pulp;
KW bleaching; ds.
XX
XX *Bacillus* sp; 1-43-3 (CBS 672.93).
XX
XX WO9518219-A1.
XX
XX 06-JUL-1995.
XX
XX 23-DEC-1994; 94WO-EP004312.
XX
XX 24-DEC-1993; 93EP-00203694.
XX
XX (KONN) GIST-BROCADES NV.
XX
XX Van Solingen P, Williams DP, Iverson S, Farrell RL, Herbes WT;
PI Van Der Kleij WA, Herwijer MA, Van Beckhoven RFWC, Quax WJ;
PI Goedegebuur F, Jones BE;
XX
XX WPI: 1995-246385/32.
DR P-PSDB; AAR76551.
XX
XX Novel xylanase enzyme active at high pH - useful in paper and pulp prodn.
PT processes.
XX
XX Claim 4; Page 42-43; 54pp; English.
XX
XX The sequence encodes an alkaline endo-1,4-beta-D-xylanase (G-type) from
CC *Bacillus* sp. 1-43-3. Fragments of the sequence (e.g. the internal
CC fragments given in AAQ92876 and AAQ92877) may be amplified by polymerase
CC chain reaction, e.g. using primers with sequences AAQ92866, AAQ92867,
CC AAQ92868 and AAQ92869. The DNA may be cloned in *Escherichia coli* using a
CC plasmid vector for recombinant xylanase production. The xylanase may be
CC used in the paper and pulp industries, where it produces an increase in
CC ISO brightness of softwood pulp of at least 1.0 over non-enzymatically
CC treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg C.
CC The enzyme may be used in production of paper, board and fluff pulp, and
CC has low cellulase activity. The increased brightness produced using the
CC xylanase allows reduction in the amount of bleaching chemicals used.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 744 BP; 248 A; 145 C; 159 G; 192 T; 0 U; 0 Other;
Query Match 94.2%; Score 624.6; DB 2; Length 744;
Best Local Similarity 96.4%; Pred. No. 1.7e-176;
Matches 639; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 CAAATCGTCACGCAAAATTCATTCGCAACGAGTGGCTATGATTAATTTGGAAA 60
DB 79 CAAATCGTCACGCAAAATTCATTCGCAACGAGTGGCTATGATTAATTTGGAAA 138
QY 61 GATAGCGGTGGCTCTCGGCAATGATTCATCATGCGGGTACGTTCAAGTCCCAATGG 120
DB 139 GATAGCGGTGGCTCTCGGCAATGATTCATCATGCGGGTACGTTCAAGTCCCAATGG 198
QY 121 AACAAATGTTAAACAATATTTTCGTAAGGTAAATAATTCATCAAAACACAAACACAC 180
DB 199 AACAAATGTTAAACAATATTTTCGTAAGGTAAATAATTCATCAAAACACAAACACAC 258
QY 181 CAAACAAGTTGGTAACATGTCCATAAATACTACGGAGCCAACTTCCAAACCAATGTAATGCG 240

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Db 259 CAACAGTTGGTAACATGTCATTAACATATGGCGCAAACTTCAGCCCAACGGTAATGCG 318
Qy 241 TATTATCGGCTATGGTGGACCTCTGTGCGAATATATATATGTCGACAGT 300
Db 319 TATTATCGGCTATGGTGGACCTCTGTGCGAATATATATATGTCGACAGT 378
Qy 301 TGGGCAACTGGCTCCACAGGACGACGCTTAAGGGACCATCTGTTGATGGAGGA 360
Db 379 TGGGCAACTGGCTCCACAGGACGACGCTTAAGGGACCATCTGTTGATGGAGGA 438
Qy 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAGGGGATTTGCCACA 420
Db 439 ACATATGATATCTAGAACTCTTAGAGTCAATCAGCCCTCCATTAGGGGATTTGCCACA 498
Qy 421 TTTAAACAATATGGAGTGTTCGAAGATCGAAACGACGAGTGGCAAGATTTCTGTGACG 480
Db 499 TTTAAACAATATGGAGTGTTCGAAGATCGAAACGACGAGTGGCAAGATTTCTGTGACG 558
Qy 481 AACCACTTTAGAGTGGGAAACCTTAGGGATGAATATGGGAAATGTATGAAGTCGCG 540
Db 559 AACCACTTTAGAGTGGGAAACCTTAGGGATGAATATGGGAAATGTATGAAGTCGCG 618
Qy 541 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 600
Db 619 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 678
Qy 601 ATTACGGTACCCCTCTCTCAACTATTAGTATGACGAGACATTAATCTTGGATAAAGAAC 660
Db 679 ATTACGGTACCCCTCTCTCAACTATTAGTATGACGAGACATTAATCTTGGATAAAGAAC 738
Qy 661 AAT 663
Db 739 AAT 741

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RESULT 7

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AAV13074
ID AAV13074 standard; DNA; 747 BP.
XX AAV13074;
AC AAV13074;
DT 19-MAY-1998 (first entry)
XX Xylanase activity positive clone DNA SEQ ID NO:11.
DE Bacillus sp; xylanase; glycosyl hydrolase family 11; isolation;
KW microorganism; identification; hybrid DNA; ss.
XX Synthetic.
OS Bacillus sp.
XX Key Location/Qualifiers
FH 1..747
FT /tag= a
FT /product= "positive clone for xylanase activity"
XX
XX WO9743409-A2.
XX
XX 20-NOV-1997.
XX
XX 12-MAY-1997; 97WO-DK000216.
XX
XX 10-MAY-1996; 96DK-00000562.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Dalboge H, Diderichsen B, Sandal T, Kauppinen S;
XX WPI; 1998-008878/01.
XX
XX Isolating novel DNA sequences from microorganisms - without the need for
XX culturing the microorganism.
FT

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XX Example 1; Page 35; 72pp; English.
PS
XX The present sequence represents a positive clone for xylanase activity
CC from an example of the present invention. The present invention describes
CC a novel method for providing a novel DNA sequence encoding a polypeptide
CC from a microorganism with an activity of interest. The method comprises:
CC (i) PCR amplification of the DNA with PCR primers with homology to (a)
CC known gene(s) encoding a polypeptide with an activity of interest; (ii)
CC linking the obtained PCR product of a 5' structural gene sequence and a
CC 3' structural gene sequence; (iii) expressing the resulting hybrid DNA
CC sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide
CC with the activity of interest or a related activity; and (v) isolating
CC the hybrid DNA sequence identified in step (iv). This method provides for
CC identification and isolation of sequences from microorganisms without
CC having to cultivate and isolate the microorganism
XX
SQ Sequence 747 BP; 236 A; 168 C; 154 G; 189 T; 0 U; 0 Other;

Query Match 76.6%; Score 507.8; DB 2; Length 747;
Best Local Similarity 85.4%; Pred. No. 1.6e-141;
Matches 566; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

Qy 1 CAATCGTCCCGGCAATTCATTTGGCAACACGATGGCTATGATTAATTTTGGAAA 60
Db 82 CAATCGTCCCGGCAATTCATTTGGCAACACGATGGCTATGATTAATTTTGGAAA 141
Qy 61 GATAGCGTGGCTCTGGGCAATTCATTTGGCAACACGATGGCTATGATTAATTTTGG 120
Db 142 GATAGCGTGGCTCTGGGCAATTCATTTGGCAACACGATGGCTATGATTAATTTTGG 201
Qy 121 AACCAATGTAAACACATATTTATTCGTTAAAGGTAAAAAATTCATAGAAACACAC 180
Db 202 AACCAATGTAAACACATATTTATTCGTTAAAGGTAAAAAATTCATAGAAACACAC 261
Qy 181 CAACAAGTTGGTAACATGTCATTAACACTAGGAGCAACTTCCACCAAAATGGTAATGCG 240
Db 262 CAACAAGTTGGTAACATGTCATTAACACTAGGAGCAACTTCCACCAAAATGGTAATGCG 321
Qy 241 TATTATTCGCTCTATGTTGGACTGTTGACCTCTTGTGCAATATATATTTGTCGACAGT 300
Db 322 TATTATTCGCTCTATGTTGGACTGTTGACCTCTTGTGCAATATATATTTGTCGATAGT 381
Qy 301 TGGGGCAACTGGCTCCACAGGAGCAACGCTTAAGGGGACCATCTCTGTTGATGGAGGA 360
Db 382 TGGGGCAACTGGCTCCACAGGAGCAACGCTTAAGGGGACCATCTCTGTTGACGGGGG 441
Qy 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAGGGGATTTGCCACA 420
Db 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAGGGGACCATCTCT 501
Qy 421 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAAGATTTCTGTGACG 480
Db 502 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAAGATTTCTGTGACG 561
Qy 481 AACCACTTTAGAGTGGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTCGCG 540
Db 562 AACCACTTTAGAGTGGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTCGCG 621
Qy 541 CTTACTGTAGAGGCTATCAAGTATGCGAAGTGTCTAATGTATATAGCAATACACTAAGA 600
Db 622 CTTACTGTAGAGGCTATCAAGTATGCGAAGTGTCTAATGTATATAGCAATACACTAAGA 681
Qy 601 ATTACGGTAAACCCCTCTCTCAACTATTAGTATGACGAGACATTAATCTTGGATAAAGAAC 660
Db 682 ATTACGGTAAACCCCTCTCTCAACTATTAGTATGACGAGACATTAATCTTGGATAAAGAAC 741
Qy 661 AAT 663
Db 742 AAT 744

```

RESULT 8

CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (iii) encoding (i) is useful for amplifying nucleic
 CC acid encoding a polypeptide having a xylanase activity which involves
 CC amplification of a template nucleic acid with a primer pair capable of
 CC amplifying (ii) or its subsequence. (i) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.
 CC This sequence encodes xylanase protein isolated from an environmental
 CC sample.

XX Sequence 1956 BP; 614 A; 384 C; 423 G; 535 T; 0 U; 0 Other;

Query Match 41.7%; Score 276.4; DB 12; Length 1956;
 Best Local Similarity 66.8%; Pred. NO. 4.9e-72;
 Matches 410; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

QY 1 CAATCGTCACCGACAATTCATTCGGCAACACACGATGGCTATGATTAATGAAATTTGGAAA 60
 DB 94 CGAATAATTTAGCAATGAGACAGGACACATGGAGGCTACGACTATGAGCTCTGGAA 153
 QY 61 GATACGGTGGCTCTGGGACAATGATCTCAATCATGCGGTAGCTTCAGTGGCCCAATGG 120
 DB 154 GA---CTACGGAAATACGATTATGAACTTAACGACGGTGGTACTTTTAGTTGTCAATGG 210
 QY 121 AACAAATGTTAAACAATATTTTCGTAAGGTAAATAATTCATGAACAAACACACAC 180
 DB 211 AGTAATATCGGTAATGCACTATTTAGAAAGGGAGAAATTTAATTCGCAAAACCTAT 270
 QY 181 CAACAAATGTTGTAACATGTCATTAACACGAGGCAATCTCCACCAAAATGGTAATGG 240
 DB 271 CAAGAAATAGGAGATATAGTAGTTGAATATGCTGTGATTCAATCCAAACGAAATTC 330
 QY 241 TATTATGCGCTATGTTGGACTGTTGACCTCTTGTGCAATATATATTATGTCACAGT 300
 DB 331 TATTGTGTGTTTACGGTTGGCAAGAAATCCACTGGTTGAATATACATTTGTAGAAAGC 390
 QY 301 TGGGCACTGGCGTCCACGAGCAACGCTTAAGGGGACCATCACTGTTGTATGGAGGA 360
 DB 391 TGGGCGAGCTGGCGTCCACTGGAGCAACACCAAGAACCATCACAGTGGTGGCGGT 450
 QY 361 ACATATGATATACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGATGCCACA 420
 DB 451 ACTTATGAATATATGAATACTACCGGGTAATATCAGCTTCCATCGATGGAATCGGACA 510
 QY 421 TTTAAACAATATGAGTGTTCGAGATCGAAACGACGAGTGGCAGCATTTCTGTACG 480
 DB 511 TTCCAAACAATATGGAGTGTTCGTATCCAAAGAAACAAAGCGGAACAATATCTGTCACT 570
 QY 481 AACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATGGGAAATATGTAAGTCGCG 540
 DB 571 GAACATTTTAAACAGTGGGAAAGATGGGCATGCGAATGGGTAAAGTATGTAAGTTGCT 630
 QY 541 CTTACTGTAGAAGGCTATCAAAAGTACGGAAGTGTCTAATGATATAGCAATACACTAAGA 600
 DB 631 CTTACCGTTGAAAGTTATCAGAGCAGTGGGTACGCTAATGATATATAAGAATGAATCAGA 690
 QY 601 ATTAACGGTAACCC 614
 DB 691 ATAGGTGCAATCC 704

RESULT 10

ID AAZ51821 standard; DNA; 2364 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

grass; paper and pulp industry; feed processing; food additive;
 plant cell wall material; degradation; ds.

OS Clostridium stercorarium.

Key Location/Qualifiers
 CDS 440..1978
 /tag= e
 /product= "Xylanase A"

WO200014243-A1.

16-MAR-2000.

03-SEP-1999; 99WO-US020304.

04-SEP-1998; 98US-0099136P.

(UYGE-) UNIV GEORGIA RES FOUND INC.

Blum DL, Kataeva I, Li X, Ljungdahl LG;

WPI; 2000-256991/22.

P-PSDB; AAY70523.

New recombinant DNA molecule comprising a sequence encoding feruloyl
 esterase protein, useful for treating grasses and other plant materials
 used in pulp and paper industries, feed processing and food additives.

Disclosure; Page 97-99; 105pp; English.

The present sequence is a DNA encoding xylanase A (XynA) from Clostridium
 stercorarium. XynA contains family VI cellulose binding domain (CBD)
 which is homologous to the CBD of xylanase Z (XynZ) of Clostridium
 thermocellum. XynZ is an enzymatic component of C. thermocellum
 cellulosome and has a multi-domain structure which includes a dockerin
 domain, a catalytic xylanase domain, a family VI cellulose binding domain
 and a domain of unknown function. The unknown domain in the N-terminal
 region of XynZ has been found to contain feruloyl (phenolic acid)
 esterase which is involved in the degradation of plant cell wall
 material. The novel feruloyl esterase is thermostable, easy to purify,
 has high temperature optima and stable over a wide pH range. The enzyme
 is useful for producing ferulic acid from wheat bran or agricultural
 byproducts, treating grasses or other plant materials used in the pulp
 and paper industries, in feed processing and as a food additive

Sequence 2364 BP; 791 A; 428 C; 458 G; 587 T; 0 U; 0 Other;

Query Match 38.5%; Score 255.4; DB 3; Length 2364;

Best Local Similarity 65.6%; Pred. No. 1e-65;

Matches 405; Conservative 0; Mismatches 206; Indels 6; Gaps 2;

QY 1 CAATCGTCACCGACAATTCATTCGGCAACACACGATGGCTATGATTAATGAAATTTGGAAA 60
 DB 533 CGAATAATTTACGACAATGAGACAGGACACATCGAGGCTACGACTATGAGCTCTGGAAA 592
 QY 61 GATACGGTGGCTCTGGGACAATGATTTCTCAATCATGCGGTACGTTCAAGTGGCCCAATGG 120
 DB 593 GA---CTACGGAAATACGATTATGGAATTAACGACGGTGGTACTTTTAGTTGTCAATGG 649
 QY 121 AACAAATGTTAAACAATATTTCCGTAAGGTAAATAATTCATGAACAAACACACACAC 180
 DB 650 AGTAATATCGGTAATGCACTATTTAGAAAGGGAGAAATTTAATTCGCAAAACCTAT 709
 QY 181 CAACAAATGTTGTAACATGTCATTAACCTACCGAGGCAACTTCCAAACCAAAATGGTAATCG 240
 DB 710 CAAGAAATTAGAGACATAGTAGTTGAATATGCTGTGATTACATCCAAACGAAATTC 769
 QY 241 TATTATGCGTCTATGTTGGACTGTTGACCTCTTGTGCAATATATATTATGTCACAGT 300
 DB 770 TATTGTGTGTTTACGGTTGGACAAGAAATCCACTGGTTGAATATTAATTTAGTAAAGC 829
 QY 301 TGGGCAACTGGCGTCCACGAGCAACGCTTAAGGGGACCATCAC---TGTTCATGGA 357

04-JUL-2000 (first entry)-

Clostridium stercorarium xylanase A DNA.
 Xylanase A; XynA; cellulosome; feruloyl esterase; phenolic acid esterase;
 thermostable; ferulic acid; wheat bran; agricultural byproduct; treat;

Db 830 TGGGCGAGTGGCTCCACCTGGAGCAACACCAAGGAACCATCACACAGTGGATGCA 889
 Qy 358 GGAACATATGATATACAGAGCTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGGC 417
 Db 890 GGTACTTATGAATATATGAACACTACCCGGGTAAATCAGCCTTCCATCGATGGAACCTGG 949
 Qy 418 ACATTTAAACATATTTGGAGTGTTCGAAGATCGAAACGACAGTGGGACAGATTTCTGTC 477
 Db 950 ACATTTCAACATATTTGGAGTGTTCGATCATCAAGAGAACCAAGCGGACATATCTGTC 1009
 Qy 478 AGCAACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATCGGGAAATGTATCAAGTTC 537
 Db 1010 ACTGACATTTTAAACAGTGGGAAAGAAATGGGCATCGGAATGGTAAAGATGTATGAAGTT 1069
 Qy 538 GGCCTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTAAATGTATATAGCAATACACTA 597
 Db 1070 GCTCTTACCGTTGAAGTGTATCAGAGCAGTGGGTACGCTTAATGTATACAAAGATGAATC 1129
 Qy 598 AGAATTAACGGTAACCC 614
 Db 1130 AGAATAGGTGCAATCC 1146

RESULT 11

AAQ80923 standard; DNA; 1022 BP.

ID AAQ80923

AC AAQ80923;

XX 02-AUG-1995 (first entry)

XX B. pumilus xylanase gene.

XX Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping; biobleaching;
 KW bleaching; Bacillus licheniformis; ss.
 XX Bacillus pumilus.

XX Key Location/Qualifiers
 FH 5'UTR 1..185
 FT /*tag= a
 FT /note= "claim 12"
 FT misc_difference 107
 FT /*tag= b
 FT /note= "base n at position 107 is not identified in the
 FT specification"
 FT CDS 186..869
 FT /*tag= c
 FT sig_peptide 186..266
 FT /*tag= d
 FT /note= "claim 11"
 FT mat_peptide 267..866
 FT /*tag= e
 FT /EC number= "3.2.1.8"
 FT /note= "claim 10"
 XX

GB2279955-A.

18-JAN-1995.

15-JUL-1993; 93GB-00014780.

15-JUL-1993; 93GB-00014780.

(SOLV) SOLVAY & CIE.

Amory A, Andre C, De Buyl E, Detroz R, Lahaye A, Ledoux P;

WPI; 1995-039214/06.

P-PSDB; AAR68849.

Purified xylanase from Bacillus pumilus PRL B12 - esp. produced in

PT transformed Bacillus licheniformis, and related DNA, vectors, etc., used
 PT for pre-treatment of wood pulp to reduce chlorine or ozone consumption in
 PT subsequent bleaching.

XX Claim 13; Fig 1a-1b; 97pp; English.

CC A Bacillus pumilus PTL B12 (ATCC 55443) gene library was screened for
 CC recombinant plasmids carrying the xylanase gene. A chromosomal fragment
 CC obtained from isolate pBPXI was subcloned and expressed in Escherichia
 CC coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3AI
 CC fragment) carried by a selected transformant is given in AAQ80923

XX Sequence 1022 BP; 329 A; 197 C; 229 G; 266 T; 0 U; 1 Other;

SQ Query Match 38.5%; Score 255.2; DB 2; Length 1022;
 Best Local Similarity 65.5%; Pred. No. 8.4e-66;
 Matches 406; Conservative 0; Mismatches 208; Indels 6; Gaps 2;
 Qy 13 GACAAATCCATTTGGCAACGATGGCTATGATATGAATTTTGGAAAGATAGCGGTGGC 72
 Db 279 GATAATAGGATAGGACACACAGCGGATACGATTTTGAATTTATGGAAGATTAC---GGA 335
 Qy 73 TCTGGGCAATGATCTCAATCATGGCGGTAGCTTCAGTGGCCCATGGAAACAATGTTAAC 132
 Db 336 AATACCTCGATGACACTCAATAACGGCGGGGCAATTTAGTGAAGCTGGAACAATATTGA 395
 Qy 133 AACATATTATTCCGTAAGAGTAAATAATTCATATGAACACAAACACCAACAAGTTGTT 192
 Db 396 AATGCTTTATTTTCGAAAGAGAAAGAGTTTGNATCCACTTAAACTCATCATCACTGGC 455
 Qy 193 AACATGTCCTAATAACTACGGAGCCAACTTCCAAACCAATGGTAATGCGTATTTATGCGTC 252
 Db 456 AACATCTCCATCAACTACAAACGAGCCTTTAAACCGGCGGGAATTCCTATTATTATGTC 515
 Qy 253 TATGTTGGAGTGTTCGACCTCTTTCGAAATATATATGTCGACAGTTGGGGCAACTGG 312
 Db 516 TATGCTGGACACAATCTCCATTAGCTGAATACTACATTTGTTGAGTCATGGGGCAATAT 575
 Qy 313 CGTCCACAGGAGCAACGCTTAAGGGGACCATCACTGTTGTATGGAGGAACATATGATATC 372
 Db 576 CGTCCACAGG---AACGTATTAAGGATCATTTTATGCCGATGGAGGCACATATGACATA 632
 Qy 373 TACGAGACTTTTAGAGTCAATCAACCTCCATTAAGGGGATTTGCCACATTTAAACAATAT 432
 Db 633 TATGAAACGCTCCGTGTCAATCAGCCTTCTATCATTTGGAGAGCGCTACCTTCAACAATAT 692
 Qy 433 TGGAGTGTTCGAAGATCGAAACGACGATGGCAGATTTCTGTCAGCAACCACTTTTGA 492
 Db 693 TGGAGTGTACGTCAAAACAAACGCAACGCGGAACGGTCTCCGTCAAGTGAAGCAATTTAAA 752
 Qy 493 GCGTGGGAAACTTTAGGATGAATATGGGAAATATGTAAGTCCGCTTACTGTAGAA 552
 Db 753 AAATGGGAAAGCTTTAGGCATGCCAATGGGAAATATGTAAGAACAGCATTAACTGTAGAA 812
 Qy 553 GGCTATCAAAGTAGCGGAAGTCTTAATGTATATAGCAATACACTAAGAAATTAACGGTAAC 612
 Db 813 GGCTACCGAAGCAACGGAAGTGCATGTGTCATGACGAATCAGCTGATGATTCGATAAAG 872
 Qy 613 CCTCTCTCAACTATTAGTAA 632
 Db 873 CATATGAAAAAAGCCAGCAA 892

RESULT 12

ADJ34969

ID ADJ34969 standard; DNA; 684 BP.

XX ADJ34969;

XX AC

XX 22-APR-2004 (first entry)

XX DNA encoding xylanase from an environmental sample seq id 185.

XX

XX

KW antibacterial; fungicide; thermostable xylanase activity;
 KW dough conditioning; beverage production; nutritional supplement;
 KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
 KW fungal infection; coccidiosis; gene; ds.
 XX Unidentified.
 XX WO2003106654-A2.
 PN 24-DEC-2003.
 XX 16-JUN-2003; 2003WO-US019153.
 XX 14-JUN-2002; 2002US-0389299P.
 XX (DIVE-) DIVERSA CORP.
 PA Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
 PI Esteghlalian A;
 XX WPI; 2004-099016/10.
 DR P-PSDB; ADJ34970.
 XX Novel xylanase recombinant polypeptide useful for improving textile
 PT texture, treating paper, eliminating microorganisms.
 XX Claim 1; SEQ ID NO 185; 570pp; English.
 XX The invention describes an isolated or recombinant polypeptide (I),
 CC having 50% or more identity to 190 300-1200 residue amino acid sequences
 CC (S1), given in the specification, over a region of 100 or more residues
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
 CC dough conditioning; beverage production; as a nutritional supplement in
 CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 CC acid encoding a polypeptide having a xylanase activity which involves
 CC amplification of a template nucleic acid with a primer pair capable of
 CC amplifying (II) or its subsequence. (I) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.
 CC This sequence encodes xylanase protein isolated from an environmental
 CC sample.
 XX SQ Sequence 684 BP; 221 A; 129 C; 158 G; 176 T; 0 U; 0 Other;
 SQ Query Match 38.5%; Score 255; DB 12; Length 684;
 Best Local Similarity 66.8%; Pred. No. 8.2e-66;
 Matches 395; Conservative 0; Mismatches 190; Indels 6; Gaps 2;
 QY 13 GACAAATCCATTGGCAACCAACGATGGCTATGATTTTGAAGAAGATAGCGTGGC 72
 DB 94 GATAATAGGATAGGACACACAGCGGATACGATTTTGAATATGAAGATTAC---GGA 150
 QY 73 TCTGGGACAATGATTCTCAATCATCGCGGTACGTTTCAGTGCCTCAATGGAACAATGTTAAC 132
 DB 151 AATACCTCGATGACACTCAATAACGCGGGCGCATTTAGTGAAGCTGGAACAATATGGA 210
 QY 133 AACATATTTCGTTAAAGGTAAATAATTCATGAACACACACACCAACCAAGTTGGT 192
 DB 211 AATGCCCTTATTTGGAAGAAGAAAGATTGATTCACATAAACAATCATCACTAATGGC 270
 QY 193 AACATGCTCAATAAATACGAGGCAACTTCCAAACCAAAATGGTAATCGGTATTTATGCGTC 252
 DB 271 AACATCTCCATCACTACAGCAGCGCTTTACCCGGGGGGAATTCCTATTATGTC 330
 QY 253 TATGGTTGACGTTTGACCCCTCTTGTGGAATATATATTTGTGCGACAGTTGGGGCAACTGG 312
 DB 331 TATGGCTGACACAAATCTCCATTAGTGAATACATTTGTTGAGTTCATGGGGGCATAT 390
 QY 313 CGTCCACAGGACGACGCTTAAGGGGACCATCTGTTGTATGGAGGAACATATGATATC 372
 DB 391 CGTCCAAACAGG---AACGTATAAAGGATCATTTTATGCCGTGGAGGCATATGACATA 447

QY 373 TACGAGACTCTTAGAGTCATCAACCTCCATTAAAGGGATTGCCACATTTAAACAATAT 432
 DB 448 TATGAACAGCTCCGTGTCATCAGCTTCTATCATTTGGAGACGCTACCTTCAACAATAT 507
 QY 433 TGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTGACGAAACCACTTTAGA 492
 DB 508 TGGAGTGTACGTCAACCAAAACGACAAAGCGGAACCTGTTTCCGTGAGTGGAGCAATTTAAA 567
 QY 493 CGGTGGGAAAACCTTAGGATGAATATGGGGAATATGTGAATATCGGCTTACTGTAGAA 552
 DB 568 AAATGGGAAAACCTTAGGATGCAATGGGGAATATGTGAATATCGGCTTACTGTAGAA 627
 QY 553 GGCTATCAAAAGTAGCGGAAGTGTATATGATATATAGCAATACACTAAGAAAT 603
 DB 628 GGCTACCGAAGCAACGGAAGTGCATGATGTCATGCAATCAGCTGATGATT 678
 RESULT 13
 AAT90972
 ID AAT90972 standard; DNA; 1190 BP.
 XX AC AAT90972;
 XX DT 22-MAY-1998 (first entry)
 XX DE Nucleotide sequence encoding an enzyme with xylanase activity.
 XX KW xynB gene; xylanase; enzyme; Dictyoglomus thermophilum strain Rt46B.1;
 KW G-xylanase; beta -1,4-xylanase activity; activity; thermal stability;
 KW biological bleaching; cellulose product; paper pulp; ss.
 XX OS Dictyoglomus thermophilum.
 XX FH Key Location/Qualifiers
 FT CDS 67..1149
 FT /tag= a
 FT /product= "xylanase"
 FT sig_peptide 67..138
 FT /tag= b
 FT mat_peptide 139..1146
 FT /tag= c
 XX WO9736995-A2.
 XX 09-OCT-1997.
 XX 27-MAR-1997; 97WO-NZ0000042.
 XX 29-MAR-1996; 96NZ-00286296.
 XX (PACI-) PACIFIC ENZYMES LTD.
 XX Bergquist PL, Gibbs MD, Morris D;
 XX WPI; 1997-503090/46.
 DR P-PSDB; AAW30267.
 XX Dictyoglomus thermophilum xylanase gene - used for producing thermally
 stable enzymes for the bleaching of cellulose products, especially paper
 pulp.
 XX Disclosure; Fig 3; 34pp; English.
 XX The present sequence represents a Rt46B.1 xynB gene and encodes a xylanase
 enzyme. The present sequence is derived from a gene contained within
 Dictyoglomus thermophilum strain Rt46B.1. The xylanase is contained
 within the family of enzymes known as G-Xylanases, and has beta -1,4-
 xylanase activity. The enzyme has high activity and high thermal
 stability with optimum activity at 85 degrees Celsius and pH 6.5. The
 xylanase enzyme is used for the biological bleaching of cellulose
 products, especially paper pulp. Use of the enzyme ensures that waste
 streams from the biological bleaching will include less toxic material
 CC

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XX 14-JUN-1994; 94EP-00201699.
XX PR
XX XX
XX PA (KONN ) GIST-BROCADES BV.
XX XX
XX GR Groenberg V, Williams DP, Iverson S, Forster S, Moody D;
XX PI Farrel RL, Bergquist PL, Daniel RM, Morgan HW, Quax WJ;
XX PI Herweijer MA, Jones BE;
XX XX
XX WFI; 1996-049690/05.
XX DR P-PSDB; AAR87012.
XX DR
XX XX
XX PT Novel xylanase(s) having activity at 80 deg.C. or higher - obtained from
XX PT anaerobic thermophilic bacteria and used in paper and pulp production
XX PT processes.
XX PT
XX XX
XX Example 9; Page 56-58; 77pp; English.
XX PS
XX PS
XX CC A full-length xynd gene (AAR08142) codes for a thermostable G-type
XX CC xylanase (AAR87012) useful in the pulp and paper industries. The gene was
XX CC obtd. by genomic walking PCR of DNA from an extremely thermophilic
XX CC bacterium, strain TG456 (CBS 213 94), isolated from a New Zealand hot
XX CC spring. The gene can be inserted into a vector and used for the prodn. of
XX CC recombinant xylanase D in microbial host cells, esp. Escherichia coli.
XX CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to
XX CC correct OS field.)
XX CC
XX CC Sequence 1244 BP; 380 A; 215 C; 279 G; 360 T; 0 U; 10 Other;
XX SQ
XX
Query Match 30.9%; Score 204.8; DB 2; Length 1244;
Best Local Similarity 61.0%; Pred. No. 1.1e-50;
Matches 367; Conservative 2; Mismatches 224; Indels 9; Gaps 2;
Qy 8 TCACCGACAATTCCATTGGCAACACCACTGGCTATGATTATGAATTTTGGAAAGATACGC 67
Db 71 TTACTCTTAATGAACTGGGACATACAGTGGTACTACTACGAGTTGTGGAGGCACAG 130
Qy 68 GTGGCTCTGGGACAAATGATTCTCAATCATGTGGCGGTACGTTTCAGTGGCCCAATGGAAACAATG 127
Db 131 GGAATACT---ACCATGACAGTTTGACACAGGAGGAAGATTTTAGCTGTGTCAGTGGAGTACAA 187
Qy 128 TTAACACATATTATTCGGTAAAGGTAAAAAATTCATAGTAAACAAACACACCAACAAG 187
Db 188 TTACAATGCACTCTTCAGAACAGGTAAAAAAGTTTAGCACTGCAATGGATCAGC----- 241

```

242	TTGGGACTGTAAAGATTAC	TCTCTCTGCTACCAATCCAAATGGCAATTCCTATCTCT	301	
Qy	248	CGCTCTATGGTTGACGTG	TGACCCCTTTGTCGAATATTATTTGTCGACAGTTGGGGCA	307
Db	302	GCATTTATGGATGGTCAAGAAATCCACTTGTGTGAATTTTATCGTTGAAAGCTGGGGCT	361	
Qy	308	ACTGGCGTCCACAGGAGCAACGCTTAAGGGACCATCACTGTGTGATGGAGGAACATATG	367	
Db	362	CATGGCGTCCGCCCGGGGCAACGTCACCTGTGCACCTGTAAACAAATTTGATGGAGCAACATATG	421	
Qy	368	ATACTACGAGACCTTTAGAGTCAATCAACCCCTCCATTTAAGGGGATTGCCACATTTTAAAC	427	
Db	422	ATATTTTAAGACAACCTCGTGTTAATCAGCCCATCTATCGAAGGAAACAAGAACATTTTGATC	481	
Qy	428	AATATTGGAGTGTTCGAAGATCGAAGACGACAGTGGCAGCATTTCTGTACGCAACCACT	487	
Db	482	AGTACTGGAGTGTTAGGACATCAAAGAGAACAGTGGTACTGTGTACTGTAACTGATCATT	541	
Qy	488	TTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAAATGTATGAAGTCGCGCTTACTG	547	
Db	542	TCAAAGCATGGGCTGCAAAAGTTTGAACCTGGGTACAAATTTGACCAGATTACACTCTGTG	601	
Qy	548	TAGAAGGCTATCAAAGTAGCGGAAGTGTAAATGTATATAGCAATACACATAGAAATTAACG	607	
Db	602	TGGAAGGYTACCARAGCAGCGGCTCAGCAAAATATAACACAGAAATACATTTACTATTTGGTG	661	

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 16:24:32 ; Search time 351.127 Seconds
(without alignments)
8406.125 Million cell updates/sec

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Perfect score: 81
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Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30.6	37.8	208	8 AQ08988	GSSTC0102
2	30.6	37.8	348	9 CC867970	NDL12311
3	30.2	37.3	449	6 CD480598	eca01-23m
4	30.2	37.3	451	4 BJ396832	BJ396832
5	29.8	36.8	663	2 BB628216	BB628216
6	29.8	36.8	1533	3 AK035636	Mus muscu
7	29.6	36.5	684	1 AV609193	AV609193
8	29.6	36.5	748	5 BX083182	EX083182
9	29.6	36.5	804	2 BE052262	GA_Ea003
10	29.6	36.5	1050	9 CNS06ROG	AL412214 T7 end of
11	29.4	36.3	706	8 BH091215	RPC1-24-3
12	29.2	36.0	498	7 CR375533	CR375533
13	29.2	36.0	623	6 CA381308	CA381308
14	29.2	36.0	780	5 BX859701	EX859701
15	29.2	36.0	824	7 CN594115	TTE000128
16	29	35.8	475	8 BZ459067	BONA064TR
17	29	35.8	480	5 BY364919	BY364919
18	29	35.8	485	5 BY365129	BY365129
19	29	35.8	588	2 BF556005	UI-R-A1-d
20	29	35.8	631	8 BH440455	BGCG06TF
21	29	35.8	762	8 BZ705274	PUBL880TD
22	29	35.8	765	7 CR371060	CR371060
23	29	35.8	810	7 CK597065	AGENCOURT
24	29	35.8	855	8 CC357397	PUHRM53TD

25	28.8	35.6	248	1 AA072982	AA072982
26	28.8	35.6	335	1 AA823781	AA823781
27	28.8	35.6	343	2 BF462060	BF462060
28	28.8	35.6	531	6 CA751489	CA751489
29	28.8	35.6	538	7 CN715895	CN715895
30	28.8	35.6	542	7 CN717635	CN717635
31	28.8	35.6	546	7 CN724716	CN724716
32	28.8	35.6	549	7 CN681450	CN681450
33	28.8	35.6	588	6 CD551944	CD551944
34	28.8	35.6	615	2 BB586000	BB586000
35	28.8	35.6	629	5 BQ770457	BQ770457
36	28.8	35.6	639	7 CF535665	CF535665
37	28.8	35.6	655	7 CF735229	CF735229
38	28.8	35.6	669	5 BM963173	BM963173
39	28.8	35.6	672	6 CB247072	CB247072
40	28.8	35.6	676	5 BU704409	BU704409
41	28.8	35.6	680	7 CN538366	CN538366
42	28.8	35.6	684	7 CK636620	CK636620
43	28.8	35.6	688	5 BQ442114	BQ442114
44	28.8	35.6	700	7 CN533101	CN533101
45	28.8	35.6	713	7 CF535405	CF535405

ALIGNMENTS

RESULT 1
AQ08988
LOCUS GSSTC010294 Trypanosoma cruzi random genomic library Trypanosoma
DEFINITION cruzi genomic clone GS1N1, genomic survey sequence.
ACCESSION AQ08988
VERSION AQ08988.3 GI:10130354
KEYWORDS GSS.
SOURCE Trypanosoma cruzi
ORGANISM Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
REFERENCE
1 (bases 1 to 208)
Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
20568489
11116034
On Sep 14, 2000 this sequence version replaced gi:9377651.
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
San Martin)
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
Aires, Argentina
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@ib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
vector.
Seq primer: T7
Class: shotgun.

FEATURES
source
1..208
/organism="Trypanosoma cruzi"
/mol_type="genomic DNA"
/strain="CL-Brener"
/db_xref="taxon:5693"
/clone="GS1N1"
/cell_type="epimastigote"
/cell_lib="Trypanosoma cruzi random genomic library"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphorylated

```

ORIGIN
  HincII site of the vector"

Query Match      37.8%; Score 30.6; DB 8; Length 208;
Best Local Similarity 65.2%; Pred. No. 33;
Matches 45; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 11 AAAGATTGAGCTGTGTTTGTGATGTATGATTGCTGCTGACACTGACGCTGTGC 70
    |||||
Db 68 ACATGTGAGGCTGTGTTTGTGATGTGTTCTTTCTGTTGAGCCGACGCTGTGTC 127
    |||||

Qy 71 CGGCTCATG 79
    |||||
Db 128 TGGATTGTG 136

RESULT 2
CC867970/c
LOCUS
DEFINITION ND.L123116.T7 Notre Dame Liverpool Aedes aegypti genomic clone
  Notredame Liverpool-123116, genomic survey sequence.
ACCESSION CC867970
VERSION CC867970.1 GI:33227980
KEYWORDS GSS
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
  Stegomyia.
REFERENCE
  1. (bases 1 to 348)
  Loftus,B., Shetty,J., Knudson,D. and Severson,D.
  BAC end sequencing of Aedes aegypti
  UNPUBLISHED (2003)
  CONTACT: Brendan Loftus
  DEPARTMENT OF Eukaryotic Genomics
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  TEL: 301-838-3543
  FAX: 301-838-0208
  EMAIL: enta@tigr.org
  LIBRARY WAS PROVIDED BY DAVID SEVERSON
  SEQ PRIMER: 17
  CLASS: BAC ends.
FEATURES
  source
    1..348
    /organism="Aedes aegypti"
    /mol_type="genomic DNA"
    /strain="Liverpool"
    /db_xref="taxon:7159"
    /clone="Notredame Liverpool-123116"
    /clone_lib="Notre Dame Liverpool"
    /note="Vector: pSCBAC1; Site_1: Hind III; The library was
    prepared from whole body tissue of newly hatched L1 larvae
    by David Severson at the University of Notre Dame and
    Hongbin Zhang"

ORIGIN
  Query Match      37.8%; Score 30.6; DB 9; Length 348;
  Best Local Similarity 73.6%; Pred. No. 36;
  Matches 39; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATTTGAAAGATTGAGGCTGTGTTTGTGATGTGTTGATTTGCTGTGCT 53
    |||||
Db 115 ATGATTTGATATATTTAGGCTGTGGATGTGATATATATTCGCTGTGAT 63
    |||||

RESULT 3
CD480598
LOCUS
DEFINITION eca01-23msl-g10 Eca01 Eschscholzia californica cDNA clone
ACCESSION CD480598
VERSION CD480598.1 GI:31401866

EST.
Eschscholzia californica (California poppy)
Eschscholzia californica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Eschscholziaceae; Eschscholzia.
1 (bases 1 to 449)
REFERENCE
  dePamphilis,C., Carlson,J., Ma,H., Tanksley,S., Field,D.,
  Leebens-Mack,J., Arrington,J., Zahn,L.M., Kong,H., Ilut,D.,
  Druckenmiller,M., Landherr,L., Hu,Y., Plock,S., Wall,K.,
  Chioorean,S., Albert,V., Doyle,J., Frohlich,M., Miller,W.,
  Oppenheimer,D., Soltis,D., Soltis,P. and Theissen,G.
  Generation of ESTs from early flower buds of Eschscholzia
  californica (2002)
  UNPUBLISHED
  CONTACT: Claude dePamphilis or James Leebens-Mack
  Mueller Laboratory
  Penn State University
  208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
  State University, University Park, PA 16802, USA
  TEL: 814 863 6413
  FAX: 814 865 9131
  EMAIL: cwd3@psu.edu or jhl10@psu.edu
  The sequence provided is trimmed of vector and low quality regions.
  Full sequence and original trace file are available from the Plant
  Genome Network website (http://pgn.cornell.edu)
  Plate: eca01-23msl row: g column: 10
  Seq primer: M13F.
  Location/Qualifiers
    1..449
    /organism="Eschscholzia californica"
    /mol_type="mRNA"
    /cultivar="Aurantia Orange"
    /db_xref="taxon:3467"
    /clone="eca01-23msl-g10"
    /tissue_type="flower buds <= 2.5mm"
    /dev_stage="millimeter buds"
    /lab_host="SOLR"
    /clone_lib="Eca01"
    /note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
    Site 2: XhoI; Plants were grown in greenhouse at Penn
    State from commercially available seeds. Only floral buds
    with diameter of 2.5 mm or less were collected. This is a
    directionally cloned, non-normalized library. Avg. insert
    length: 1702; Primers: M13F and M13R; Antibiotic: 50 ug/ml
    Ampicillin; Primary Titer: 7E6 pfu total; Amplified Titer:
    1.8E11 pfu/ml; Mass Excised Titer: 5.6E8 total; This
    library has been generated by the Floral Genome Project
    (FGP). We would like to thank Huck Life Sciences
    Consortium for their assistance. The Floral Genome Project
    is funded by NSF's Plant Genome Research Program
    (DBI-0115684). More information about the project can be
    obtained at http://fgp.bio.psu.edu"

ORIGIN
  Query Match      37.3%; Score 30.2; DB 6; Length 449;
  Best Local Similarity 65.7%; Pred. No. 51;
  Matches 44; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 6 TTTGAAAAGATTGAGGCTGTGTTTGTGATGTGTTGATTTGCTGACACGACGCG 65
    |||||
Db 223 TTTGAGCTGATGTGATCTATAAAATGTGATCTTGAAACGATATGCTGACGCTTCT 282
    |||||

Qy 66 TGTGCGG 72
    |||||
Db 283 TGTGCTG 289

RESULT 4
BU396832/c
LOCUS
DEFINITION BU396832 Dictyostelium discoideum cDNA library, SF Dictyostelium
  discoideum cDNA clone dds4j03 5', mRNA sequence.
  451 bp mRNA linear EST 08-MAR-2002

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[illegible]


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QY      63 GGCTGTGC 70
      |||||
Db      201 GGGTGTTC 208

RESULT 8
BX083182
LOCUS
DEFINITION
BX083182 AGENAE Rainbow trout normalized multi-tissues library
(tcac) Oncorhynchus mykiss cDNA clone tcac0004c.f.24 3prim, mRNA
sequence.
ACCESSION
BX083182
VERSION
BX083182.2 GI:42607344
KEYWORDS
EST.
SOURCE
Oncorhynchus mykiss (rainbow trout)
ORGANISM
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
1 (bases 1 to 748)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Jan 14, 2003 this sequence version replaced gi:27746599.
JOURNAL
Contact: Guiguen Y
COMMENT
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0004 row: f column: 24
Seq primer: T3.
FEATURES
Location/Qualifiers
source
1..748
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcac0004c.f.24"
/tissue types="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="AGENAE Rainbow trout normalized multi-tissues
library (tcac)"
/note="vector: pT73D-pac; Clone distribution : AGENAE
Resource centre, Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Query Match 36.5%; Score 29.6; DB 5; Length 748;
Best Local Similarity 64.7%; Pred. No. 86;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY      2 TGAATTGAAAGATTGAGCTGTTTGTGTGATGTATGATTTGCTGCACTGA 61
      |||||
Db      245 TGCACAGGGAAGCGGCAGCTGCTGTGGTGTGATGGTGGGTGTTGTGGCCTGA 304
      |||||

QY      62 CGGCTGTG 69
      |||||
Db      305 CCTGTGTG 312
      |||||

RESULT 9
BE052262
LOCUS
DEFINITION
GA_Ea0035L23f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0035L23f, mRNA sequence.
ACCESSION
BE052262
VERSION
BE052262.2 GI:13246906
KEYWORDS
EST.
SOURCE
Gossypium arboreum
ORGANISM
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE
1 (bases 1 to 804)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
On Jun 8, 2000 this sequence version replaced gi:8379318.
JOURNAL
Contact: Wing RA
COMMENT
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 2
High quality sequence stop: 475.
High quality sequence start: 475.
High quality sequence stop: 475.
FEATURES
Location/Qualifiers
source
1..804
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0035L23f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 36.5%; Score 29.6; DB 2; Length 804;
Best Local Similarity 73.1%; Pred. No. 88;
Matches 38; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      3 GAATTTGAAAGATTGAGCTGTTTGTGTGATGTATGATTTGCTGCTG 54
      |||||
Db      474 GACTTTGATAAGCATGAGGATCTTGTGAGTGAATGTATAGGATTGAGCGG 525
      |||||

RESULT 10
CNS06ROG
LOCUS
DEFINITION
T7 end of clone AW0AA016B08 of library AW0AA from strain CLIB 89 of
Yarrowia lipolytica, genomic survey sequence.
ACCESSION
AL412214
VERSION
AL412214.1 GI:12182513
KEYWORDS
GSS.
SOURCE
Yarrowia lipolytica
ORGANISM
Yarrowia lipolytica
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
REFERENCE
1 (bases 1 to 1050)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Boltelin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malbertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
JOURNAL

```

```

MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 1050)
AUTHORS Casaregola,S., Neuvéglise,C., Lepingle,A., Bon,E., Peynerol,C.,
Artiguenave,F., Wincker,P. and Gaillardin,C.
TITLE Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
lipolytica
JOURNAL FEBS Lett. 487 (1), 95-100 (2000)
MEDLINE 20584727
PUBMED 11152892
REFERENCE 3 (bases 1 to 1050)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
source
Location/Qualifiers
1..1050
/organism="Yarrowia lipolytica"
/mol_type="genomic DNA"
/strain="CUB 89"
/db_xref="taxon:4952"
/clone="AW0AA016B08"
/clone_lib="AW0AA"
/note="end : 17"
<424..1047
/misc_feature
/note="similar to Saccharomyces cerevisiae ORF YLR068w [
hypothetical protein ]
1 putative frameshift(s)"
/evidence=not_experimental
ORIGIN
Query Match 36.5%; Score 29.6; DB 9; Length 1050;
Best Local Similarity 64.7%; Pred. No. 92;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 9 GAAAGATTGAGCGCTGTTGTTGATGTGATGTTGATGTTGCTGACATGACGCGTGT 68
Db 577 GACAAGCTGAGACTGTTGAGAAGCTGAGGATGAGTCTGGAGATGAATCTGAGGCTCT 636
QY 69 GCGGCTC 76
Db 637 GCGGCTC 644
RESULT 11
BH091215/c
LOCUS BH091215
DEFINITION RPCI-24-356N3.TJ RPCI-24 Mus musculus genomic clone RPCI-24-356N3,
genomic survey sequence.
ACCESSION BH091215
VERSION BH091215.1 GI:14911120
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 706)
REFERENCE
AUTHORS Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished (1999)
Other GSSs: RPCI-24-356N3.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 356 row: N column: 3
Seq primer: SP6
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..706
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-356N3"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."
ORIGIN
Query Match 36.3%; Score 29.4; DB 8; Length 706;
Best Local Similarity 60.8%; Pred. No. 99;
Matches 48; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGAATTTGAAAGATTGAGCGCTGTTGTTGATGTGATGTTGATGTTGCTGACACTG 60
Db 556 AAGAAATTTTAAATTTTATTTGTTTATTTATGTCATGTCGTTGTCGCGAATGT 497
QY 61 ACGCTGTGCGGCTCATG 79
Db 496 ACGTCTGTGAAGGCACGTG 478
RESULT 12
CR375533
LOCUS CR375533
DEFINITION CR375533 AGENAE Rainbow trout normalized testis library (tcbl)
Oncorhynchus mykiss cdna clone tcbl0018c.d.16 5prim, mRNA sequence.
ACCESSION CR375533
VERSION CR375533.1 GI:46501098
KEYWORDS EST.
SOURCE EST.
ORGANISM Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 498)
REFERENCE
AUTHORS Govoroun,M., Guiguen,Y. and Le Gac,F.
TITLE Construction and primary characterization of normalized cdna
libraries in rainbow trout, Oncorhynchus mykiss
JOURNAL Unpublished (2003)
COMMENT Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signauesupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

```

Plate: 0018 row: d column: 16
 Seq primer: M13R. Location/Qualifiers
 1. .498

FEATURES

source
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="tcbi0018c.d.16"
 /tissue_type="testis"
 /lab_host="DH10B"
 /clone_lib="AGENAE Rainbow trout normalized testis library (tcbi)"
 /note="Vector: pT7T3D-pac; Clone distribution : AGENAE Resource centre: Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

ORIGIN

Query Match 36.0%; Score 29.2; DB 7; Length 498;
 Best Local Similarity 62.2%; Pred. No. 1.1e+02;
 Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 QY 1 ATGAATTTGAAAGATTGAGCGCTGTTGTTGATGCTGATTGCTGACACTG 60
 |||||
 Db 378 ATGAAGAGGAGAGACTGAGCGCTATGCGCTCGCTGTGCTTACATTGAGTCAGACCTG 437
 QY 61 ACGGCTGTGCCGCG 74
 |||||
 Db 438 CCAACCGTGACCGC 451

RESULT 13

CA381308 623 bp mRNA linear EST 06-NOV-2002
 LOCUS 660794 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT55A08_C_A04 5',
 mRNA sequence.
 CA381308
 CA381308.1 GI:24703798
 EST.
 Oncorhynchus mykiss (rainbow trout)
 Oncorhynchus mykiss

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 623)

REFERENCE
 AUTHORS Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,
 Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
 Title Sequence analysis of a rainbow trout cDNA library and creation of a
 gene index

JOURNAL
 COMMENT CytoGenet. Genome Res. 102 (1-4), 347-354 (2003)
 Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351

Email: crexroad@nccwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified by
 cross_match v0.990329
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 Db 479 ATGAAGAGGAGAGACTGAGCGCTATGCGCTCGCTGTGCTTACATTGAGTCAGACCTG 538
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 Db 539 CCAACCGTGACCGC 552

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 LOCUS BX859701 AGENAE Rainbow trout normalized testis library (tcbi)
 DEFINITION Oncorhynchus mykiss cDNA clone tcbi0012d.c.19 5prim, mRNA sequence.
 ACCESSION BX859701
 VERSION BX859701.2 GI:42756450
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 780)
 REFERENCE Govoroun, M., Guiguen, Y. and Le Gac, F.
 AUTHORS Construction and primary characterization of normalized cDNA
 TITLE libraries in rainbow trout, Oncorhynchus mykiss
 JOURNAL Unpublished (2003)
 COMMENT On Dec 16, 2003 this sequence version replaced gi:39957467.
 Contact: Guiguen Y
 INRA - SCRIBE
 Campus de beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at signenasupport@jouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0012 row: c column: 19
 Seq primer: M13R. Location/Qualifiers
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FEATURES

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ORIGIN

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 Best Local Similarity 62.2%; Pred. No. 1.2e+02;
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spleen, muscle, and kidney."

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 10, 2004, 21:26:43 ; Search time 423.895 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues
Total number of hits satisfying chosen parameters: 7222084

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	119.4	18.0	1375	9	US-09-770-621-1
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9	115.2	17.4	596	15	US-10-307-441-39
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14	104.8	15.8	712	14	US-10-213-990-64	Sequence 64, Appl
15	103.6	15.6	666	14	US-10-213-990-65	Sequence 65, Appl
16	96.8	14.6	739	14	US-10-213-990-67	Sequence 67, Appl
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18	84.2	12.7	1023	16	US-10-244-596-6	Sequence 6, Appli
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20	83.2	12.5	645	15	US-10-237-386-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1
US-09-909-207-1
; Sequence 1, Application US/0909207
; Patent No. US20020145181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUMA
; PIERRE LEDOUX
; RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/909,207
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136

Patent No. US20020115181A1
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
ERIC DE BUVL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/909,207
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:

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RESULT 3

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; Sequence 4, Application US/0909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAN BRINKS HOPFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,207
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625

; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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RESULT 4

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; Sequence 5, Application US/0909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE

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ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
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FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..81
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-909-207-5
Query Match 100.0%; Score 663; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.6e-183; Indels 0; Gaps 0;
Matches 663; Conservative 0; Mismatches 0;
1 CAAATCGTCACCGACAATTCATTTGGCAACACGATGGCTATGATTGAAATTTGGAAA 60
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Db 322 TATTTATGCGCTCTATGCTTGGAGCTGTGACCCCTTGTGCGAATATATATTTGTCGAGT 381
Qy 301 TGGGGCAACTGGCGTCCACCAGGAGCAACCGCTTAAGGGGACCACATCACTGTTGATGGAGG 360
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Qy 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCAATTAAGGGGATTCGCACA 420
Db 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCAATTAAGGGGATTCGCACA 501
Qy 421 TTTAAACAATATTGGAGTGTTCGAAGATCGAAGCGACGAGTGGCAGATTTCTGTGTCAGC 480
Db 502 TTTAAACAATATTGGAGTGTTCGAAGATCGAAGCGACGAGTGGCAGATTTCTGTGTCAGC 561
Qy 481 AACCACTTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGGGAAAATGTATGAAGTCGCG 540
Db 562 AACCACTTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGGGAAAATGTATGAAGTCGCG 621
Qy 541 CTTACTGTAGAAGCTATCAAAAGTAGCGGAAGTCTTAATGTATATAGCAATACACTAAGA 600
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Qy 661 AAT 663
Db 742 AAT 744
RESULT 5
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; Sequence 10, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,207
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625

```


TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-909-207-10

Query Match 100.0%; Score 663; DB 9; Length 1513;
Best Local Similarity 100.0%; Pred. No. 2.2e-183;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTCACCGACAATTCCTATGGCAACACGATGGCTATGATTATGAATTTTGGAAA 60
DB 701 CAAATCGTCACCGACAATTCCTATGGCAACACGATGGCTATGATTATGAATTTTGGAAA 760

QY 61 GATAGCGGTGGCTCTGGGACAATGATTCCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 120
DB 761 GATAGCGGTGGCTCTGGGACAATGATTCCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 820

QY 121 AACAAATGTTAAACAATATATTCCTGTAAGGTAAAGTAAATTCATGAAACACAAACACAC 180
DB 821 AACAAATGTTAAACAATATATTCCTGTAAGGTAAAGTAAATTCATGAAACACAAACACAC 880

QY 181 CAACAAGTTGGTAACAATGTCATAAACTACGAGGCCAACTTCCAAACCAATGTAATGG 240
DB 881 CAACAAGTTGGTAACAATGTCATAAACTACGAGGCCAACTTCCAAACCAATGTAATGG 940

QY 241 TATTTATGCGCTATGCTGGTGGACTGTGACCCCTCTTGTGCAATATATATTTGTCGACGT 300
DB 941 TATTTATGCGCTATGCTGGTGGACTGTGACCCCTCTTGTGCAATATATATTTGTCGACGT 1000

QY 301 TGGGGCAACTGGCGTCCACGAGGCAACGCCCTAAGGGACCATCACTGTTGATGGAGGA 360
DB 1001 TGGGGCAACTGGCGTCCACGAGGCAACGCCCTAAGGGACCATCACTGTTGATGGAGGA 1060

QY 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGATGGCACA 420
DB 1061 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGATGGCACA 1120

QY 421 TTTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGCAAGTGGCGACGATTTCTGTCAGC 480
DB 1121 TTTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGCAAGTGGCGACGATTTCTGTCAGC 1180

QY 481 AACCACTTTAGAGGTGGGAAAATCTTAGGATCAATATGGGAAAATGATGATGAGTCGCG 540
DB 1181 AACCACTTTAGAGGTGGGAAAATCTTAGGATCAATATGGGAAAATGATGATGAGTCGCG 1240

QY 541 CTCTACTGTAGAGCTATCAAGTACGAGGAGTCTTAATGATATAGCAATACACTAAGA 600
DB 1241 CTCTACTGTAGAGCTATCAAGTACGAGGAGTCTTAATGATATAGCAATACACTAAGA 1300

QY 601 ATTAACCGGTAAACCCCTCTCAACTATTAGTAATGACGAGAGCAATACTTTGGATAAAAC 660
DB 1301 ATTAACCGGTAAACCCCTCTCAACTATTAGTAATGACGAGAGCAATACTTTGGATAAAAC 1360

QY 661 AAT 663
DB 1361 AAT 1363

RESULT 6
US-09-909-207-11
; Sequence 11, Application US/0909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE

ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: 620..1363
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 701..1363
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 620..700
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-909-207-11

Query Match 100.0%; Score 663; DB 9; Length 1513;
Best Local Similarity 100.0%; Pred. No. 2.2e-183;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAATCGTCACCGACAATTCCTATGGCAACACGATGGCTATGATTATGAATTTTGGAAA 60
DB 701 CAAATCGTCACCGACAATTCCTATGGCAACACGATGGCTATGATTATGAATTTTGGAAA 760

QY 61 GATAGCGGTGGCTCTGGGACAATGATTCCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 120
DB 761 GATAGCGGTGGCTCTGGGACAATGATTCCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 820

QY 121 AACAAATGTTAAACAATATATTCCTGTAAGGTAAAGTAAATTCATGAAACACAAACACAC 180
DB 821 AACAAATGTTAAACAATATATTCCTGTAAGGTAAAGTAAATTCATGAAACACAAACACAC 880

QY 181 CAACAAGTTGGTAACAATGTCATAAACTACGAGGCCAACTTCCAAACCAATGTAATGG 240
DB 881 CAACAAGTTGGTAACAATGTCATAAACTACGAGGCCAACTTCCAAACCAATGTAATGG 940

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881 CAACAAAGTTGGTAACATGTCCTCAATAAATACGAGGCAACCTTCCACCAAAATGGTATCGG 940
241 TATTATATGCGTCTATGGTTGGACTGTTGACCCCTTTGTCGAATATATATTTGTCGACAGT 300
941 TATTATATGCGTCTATGGTTGGACTGTTGACCCCTTTGTCGAATATATATTTGTCGACAGT 1000
301 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGGACCATCACTGTTGATGAGGA 360
1001 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGGACCATCACTGTTGATGAGGA 1060
361 ACATATGATATACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTCGCCACA 420
1061 ACATATGATATACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTCGCCACA 1120
421 TTTAAACATATGCGAGTTCGAGAGTCAACGAGGCAACGAGTGGGACCATTTCTGTCAGC 480
1121 TTTAAACATATGCGAGTTCGAGAGTCAACGAGGCAACGAGTGGGACCATTTCTGTCAGC 1180
481 AACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATGGGAAATGTATGAAGTCGCG 540
1181 AACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATGGGAAATGTATGAAGTCGCG 1240
541 CTTACTGTAGAAGGCTATCAAAAGTAGCGGAAGTGTATATATAGCAATACACTAAGA 600
1241 CTTACTGTAGAAGGCTATCAAAAGTAGCGGAAGTGTATATATAGCAATACACTAAGA 1300
601 ATTAACGGTAACCCCTCTCAACTATTAGTATGACGAGGCAATCACTTTGGATATAAAC 660
1301 ATTAACGGTAACCCCTCTCAACTATTAGTATGACGAGGCAATCACTTTGGATATAAAC 1360
661 AAT 663
1361 AAT 1363

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RESULT 7

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US-09-770-621-1
; Sequence 1, Application US/09770621
; Patent No. US20010024815A1
; GENERAL INFORMATION:
; APPLICANT: M ntyl, Arja
; APPLICANT: Vehmanper, Jari
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lahtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,621
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/590,563
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugaisky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 1050.0340003
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: No. US20010024815A1 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 303..1334
; US-09-770-621-1

Query Match      18.0%; Score 119.4; DB 9; Length 1375;
Best Local Similarity 57.1%; Pred. No. 3.8e-24;
Matches 238; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 198 GTCATTAACATACGAGGCAACCTTCCAAACCAATGGTAATGCGTATTTATGCGTCTATGG 257
DB 608 GACCGTGACCTTACAAACGCTCTTCAACCCGCTCGGGTAACGGCTACCTCAGCTCTACGG 667
QY 258 TTGCACTGTTGACCCCTCTTGTGCAATATATATTTGTCGAGTGGGCAACTGGCGTCC 317
DB 668 CTGACCAGGAAACCCGCTCGTCTGAGTACTACATCGTCTGAGAGCTGGGGACCTACCGGCC 727
QY 318 ACCAGGAGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGA 377
DB 728 CACCGG--CACCTTACAAGGGGACCGTCAACCCGCGGGGAAACGTAACGACATCTACGA 784
QY 378 GACTCTTAGAGTCAATCAACCTCCATTAAGGGGATGCCACATTTAAACATATTGGAG 437
DB 785 GACCTGGCGGTACAAACGCGCGCTCCATCGAGGGGACCCGCGGAGCTTCCAGCAGTTCTGGAG 844
QY 438 TGTTCGAAGATCGAAACGCGACGAGTGGCAGCATTTCTGTCAGCAACACCTTTAGAGCGTG 497
DB 845 CGTCCGCGCAGGAGGAGGCGGACCGGCAACCATCACCATCGGCAACCATCTCGAGCGCTG 904
QY 498 GGAATACTTAGGGATGAATATGGGGAATAATGTATGAAGTCCGCTTACTGTAGAGGCTA 557
DB 905 GGCCCGCGCGGATGAACCTGGGCGACGCACTACCATCATGGGCGACCGAGGCTA 964
QY 558 TCAAGTAGCGGAGTGTCTAATGTATATAGCAATACACTAAGATTAACGTAACCC 614
DB 965 CCAGAGCAGCGGTAGTCTCCACCGCTCCATCAGCGGGTGGCAACCCCGGCAACCC 1021

RESULT 8
US-10-286-993-1
; Sequence 1, Application US/10286993
; Publication No. US20030148453A1
; GENERAL INFORMATION:
; APPLICANT: Mantlya, Arja
; APPLICANT: Paloheimo, Marja
; APPLICANT: Lantto, Raija
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Vehmanpera, Jari
; TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
; FILE REFERENCE: 1716.0340004
; CURRENT APPLICATION NUMBER: US/10/286,993
; CURRENT FILING DATE: 2002-08-13

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; PRIOR APPLICATION NUMBER: US/09/120,804
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/FI97/00037
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: US 08/590,563
; PRIOR FILING DATE: 1996-01-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Actinomadura flexuosa (Strain: DSM43186)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (303)...(1337)
; OTHER INFORMATION: Product= AM35 xylanase
US-10-286-993-1

Query Match      18.0%; Score 119.4; DB 15; Length 1375;
Best Local Similarity 57.1%; Pred. No. 3.8e-24;
Matches 238; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 198 GTCCATAAACTACGGAGCCAACTTCCAAACCAATGGTAATGCTATTTATGCGTCTATGG 257
DB 608 GACCGTGACCTACAAACGCTCTCTTCAACCGCTCGGCTAACGGCTACCTCACGCTCTACGG 667

QY 258 TTGGAGCTGTGACCTCTTGTGCAATATTATTTGCGACAGTTGGGGCAACTGGCGTCC 317
DB 668 GTGGACCAAGAACCCCTCGTTCAGTACTACATCGTCGAGAGCTGGGGCACTTACCGGCC 727

QY 318 ACCGAGGCAACGCTTAAGGGGACCATCACTGTTGATGAGGGAACATATGATATCTACGA 377
DB 728 CACCGG---CACCTCAAGGGGACCGCTCACCCAGCGGGGAGCTAGACATCTACGA 784

QY 378 GACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTCGCACATTTTAAACAATTTGGAG 437
DB 785 GACCTGGGTACAAACGCGCGTCCATCGAGGSCACCCGACCTTCCAGCAGTTCTGGAG 844

QY 438 TGTTCAAGATCGAAACGCGAGTGGCGAGATTTCTGTGACGAAACCATTTAGACGCTG 497
DB 845 CGTCCGGCAGCAGAGCGGACCAAGCGGACCATCAGCTCGGCAACCACTTCGACGCTG 904

QY 498 GGAACACTTAGGATGATATATGGGAAATGTATGATGAGTCGCGCTTACTGTAGAGGCTA 557
DB 905 GCGCCGCGCGGATGAACCTGGGCGACGACGACTACAGATCATGGGACCGAGGCTA 964

QY 558 TCAAAGTAGCGGAGTGTCTAATGTATATAGCAATACACTAAGAAATTAACGGTAACCC 614
DB 965 CGAGACGCGGTAGTCTCCACCTCTCCATCAGGAGGCTGGCAACCCCGCAACCC 1021

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RESULT 9
US-10-307-441-39
; Sequence 39, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Trx
US-10-307-441-39

Query Match      17.4%; Score 115.2; DB 15; Length 596;
Best Local Similarity 57.7%; Pred. No. 4.3e-23;
Matches 226; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

QY 193 AACATGTCATAAACTACGGAGCCAACTTCCAAACCAATGGTAATGCGTATTTATGCGTC 252
DB 191 AATAAGGTGATCAACTTCTCGATCTTATAATCCGAATGGGAATTCATACITTAAGCGTC 250

QY 253 TATGTTGGAGCTGTTGACCTCTTTCGAAATATTATTTGTCGACAGTTGGGGCACTGG 312
DB 251 TATGCTGCTCTAGAAACCCCACTGATTGAATATTATTTGTCGAAATTTTCGGTACCTAC 310

QY 313 CGTCC---ACCAGGAGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGAACATATGAT 369
DB 311 AATCCGAGTACCGCGGCCACAAATTAGCGGAAGTCACTAGTGTGATCCGTTATGAT 370

QY 370 ATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAAGGGGATTCGCCACATTTAAACAA 429
DB 371 ATCTACCGTACCAACGCGTTAATCAGCATCGATTCATTTGGAACCGCCACCTTTTATCAG 430

QY 430 TATTGGAGTGTTCGAAGATCGAAACGCGAGTGGCAGCATTTCTGTCTAGCAACCACTTT 489
DB 431 TACTGGAGTGTTCGAGCTAATCATCGGAGCTCCGGTTCGGTTAACTACTCGGAATCACTTT 490

QY 490 AGAGCGTGGGAAACTTAGGATGAATATGGGAAATGTATGAACTCGGCTTACTGTA 549
DB 491 AATGATCGGCAACGCAAGGTTAACCTTAGGTACAATGGATATCAAAATCGTAGCGGTG 550

QY 550 GAAGCTATCAAGTAGCGGAAGTGTCTAATGT 581
DB 551 GAAGGCTACTTCTCGAGTGTTCGCGTAGTAT 582

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RESULT 10
US-10-213-990-71
; Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(942)
US-10-213-990-71

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Query Match      16.8%; Score 111.4; DB 14; Length 942;
Best Local Similarity 57.0%; Pred. No. 6.9e-22;
Matches 224; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

QY 182 AACAAAGTTGGTAACATGTCATAACTACGAGCGCCAACTTCCAAACCAATGGTAATCGGT 241
DB 257 ATCCAGGAGTGACCATGACATTTACCTTCTCTGGAGCTTCAATCTTCCGGAATGCTT 316

QY 242 ATTTATGCGTCTATGTTGACCTTGTGACCTTGTGCAATATTTATTTGTCGACAGTT 301
DB 317 ACCTGTCGCTGATGATGATGAGTACTACCAACCCCTAGTTCGAATATCTACTACTCTCGAAGT 376

```

QY 302 GGGCA---ACTGGCGTCCACGAGCAACGCTTAAGGGACCATCATCTGTTGATGAG 358
Db 377 ATGGCAGTTACAATCCTGGCTCGGCATGACGCAACAGGGCACCGCTCACCGAGGATGAT 436
QY 359 GAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGATTGCCA 418
Db 437 CCACCTACGACATCTATGACGACCAACAGGTCAACAGCCTTCGATCTGGCAGCGCA 496
QY 419 CATTAAACAATATTGGAGTGTGGAAGATCGAAACGACGAGTGGCAGCATTTCTGTCA 478
Db 497 CTTTCAACCAATACTGGTCCATCCGCCAAAACAAGCGATCCAGCGGCACAGTCAACACCG 556
QY 479 GCAACCACTTAGAGCGTGGGAACTTAGGATGAATATGGGAAATGTATGAAGTCG 538
Db 557 CGAATCACTCAAGGCCTGGGTAGTCTGGGGATGAACCTGGGTACCCATAACTATCAGA 616
QY 539 CGCTTACTGTAGAAGGCTATCAAGTAGCGGAA 571
Db 617 TTGTTTCCACTGAGGGATATGAGACAGCGGTA 649

RESULT 11

US-10-213-990-70
; Sequence 70, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Bussey, Reg
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-70

Query Match 16.6%; Score 110; DB 14; Length 1002;

Best Local Similarity 57.8%; Pred. No. 1.8e-21;
Matches 216; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

QY 201 CATAAATACGGAGCAACTTCCAAACCAAAATGGTAATGGTATTTATGCGTCTATGGTTG 260
Db 336 CATTACCTTCTGCGAGGTTCAATCCTTCGGAAATGTTACCTGTCGGTGTATGGATG 395
QY 261 GACTGTGACCTCTTGTGGAATATATATGTCGACAGTTGGGCA---ACTGGCGTCC 317
Db 396 GACTACCAACCCCTAGTTCGAATACTACATCTCGAGAATATGCGAGTTACAACTCTGG 455
QY 318 ACCAGGCAAGCCTTAAGGAGCACTCATCTGTTGATGGAGAAATATATATATCA 377
Db 456 CTCGGGCATGACGCAACAGGGCACCGCTCACAGCGATGGATCCACTAGCATCTATGA 515
QY 378 GACTCTTAGAGTCAATCAACCTTCAATTAAGGGGATGCGCATTTAAACAATATTGGAG 437
Db 516 GCACCAACAGGTCAACGAGCTTCGATCGTCGACGCGCACCTTCAACCAATATGTC 575
QY 438 TGTTTGAAGATCGAAACGCAAGTGGACGATTTCTGTTCAGCAACCACTTTAGAGCGTG 497
Db 576 CATCGGCCAAAACAAGCGATCCAGGGCACAGTCAACCCGCGAATCACTTCAAGGCCTG 635
QY 498 GGAACACTTAGGATCAATATCGGGAATATGATGAAGTCGCGCTTACTAGAGAGGCTA 557
Db 636 GCGTAGTCTGGGGATGAACCTGGGTACCCATAACTATCAGATTGTTTCCACTGAGGGATA 695
QY 558 TCAAGTAGCGGAA 571

Db 696 TGAGAGCAGCGGTA 709

RESULT 12

US-10-213-990-68
; Sequence 68, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Bussey, Reg
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(705)
US-10-213-990-68

Query Match 16.4%; Score 108.8; DB 14; Length 705;

Best Local Similarity 51.9%; Pred. No. 3.5e-21;
Matches 298; Conservative 0; Mismatches 267; Indels 9; Gaps 2;

QY 6 CGTACCAGCAATTCCTATTGGCAACCCAGCATGGCTATGATGATTAATTTTGGAAACATAG 65
Db 120 CGGCACCCCAAGCTCCACCGCTGGAAACAACGGCTACTACTCTCTTCTGGACTGATGG 179
QY 66 CGGTGGCTCTCGGCAATGATTCTCAATCATGCGGTACGTTTCAGTGCCTCCCAATGGAACA 125
Db 180 CGGCGGCGACGTGACCTACCAATGGCGCGGTGGCTGCTACTCCGTCACCTGAGGAGAA 239
QY 126 TGTTAAACAACATATTTATTCGTAAGGTAAATAATTCATGAAACACACAAACACACAA 185
Db 240 CGTGGGCAACTTTGTGCGTGGAAAGGGC-----TGGAAACCTCGAAGCGGTAGGTACCG 293
QY 186 AGTTGGTAACTGTCATATAAAGTACGAGGCAACTTCCAAACCAATGTAATGCTATTT 245
Db 294 AGCTTTAAGTAGAACCATCAACTACGGAGGAGCTTCAACCCGAGCGCAATGGCTACCT 353
QY 246 ATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTATATTGTCGACAGTTGGGG 305
Db 354 GGCTGTCTACCGCTGGACCAACCCCTTGATTTGATGACTACGTTGTTGATGCTATGG 413
QY 306 CA---ACTGGCGTCCACGAGGCAACCGCTAAGGGGACCATCACTGTTGATGGAGGAAC 362
Db 414 TACATACAACCCCGCAGCGGTACTCTTCAGGGGCACCTGTCAACACCGCGGTGGCAC 473
QY 363 ATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGATGCCACATT 422
Db 474 TTACAACATCTACAGCGCGGTTTCGCTACAATGCTCCCTCCATCGAAGGCAACCAAGACCTT 533
QY 423 TAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCGACGATTTCTGTGAGCAA 482
Db 534 CACCCAGTACTGTTCTGTGCGCACCTTCAAGGCTACCGCGGCACTGTCAACCATGGCCAA 593
QY 483 CCACCTTTAGCGTGGGAAAACCTTAGGATGAATATGGGAAATATGATAGTCCGCT 542
Db 594 CCACCTTCAACGCTGGAGCAGACTGGGCATGAACCTGGGAACTCACAACCTACAGATTGT 653
QY 543 TACTGTAGAAAGCTATCAAGTAGCGGAGTGCT 576
Db 654 CGCCACTGAGGGTTACCGAGAGCGGATCTGCT 687

RESULT 13

US-10-299-393-1
; Sequence 1, Application US/10299393
; Publication No. US20030108642A1
; GENERAL INFORMATION:
; APPLICANT: Sabatier, Alain
; APPLICANT: Fish, Neville Marshall
; APPLICANT: Haigh, Nigel Paterson
; TITLE OF INVENTION: PENICILLIUM FUNICULOSUM STRAIN USEFUL
; TITLE OF INVENTION: FOR THE PRODUCTION OF ENZYMES
; FILE REFERENCE: A32917-PCT-USA-1 (072667.0183)
; CURRENT APPLICATION NUMBER: US/10/299,393
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 09/462,246
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: EPO 9801161.5
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2898
; TYPE: DNA
; ORGANISM: Penicillium funiculosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1317)...(1589)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1590)...(1642)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1644)...(2042)
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (570)...(576)
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (724)...(730)
US-10-299-393-1

Query Match 16.0%; Score 106; DB 15; Length 2898;

Best Local Similarity 56.5%; Pred. No. 4.5e-20;

Matches 218; Conservative 0; Mismatches 165; Indels 3; Gaps 1;

QY	195	CATGTCATAAACTACGAGCCAACTTCCAAACCAATGGTAATGCGTATTATGCGTCTA	254
DB	1640	CAGGACTGTACGTAATCAGGAGAAATTAACCCCTCTGGAAACGCTTATTGGCTGTCTA	1699
QY	255	TGGTGGACTGTGACCCCTCTTGTGCAATATATATGTCGACAGTTGGGGCAACTGGCG	314
DB	1700	CGGGTGACAAACAGATCCTCTTGTGCAATATATATCTCTGAGTCTTACGCGCACTATA	1759
QY	315	TCCACCA---GGACCAACGCTAAGGGGACCATCCTCTGATGCGAGGAACATATGATAT	371
DB	1760	CCCATCATCTGGAATCTACTTCACTTGGCAGGTCACTAGCATGGTGGCACTACGATAT	1819
QY	372	CTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGCGCACTTTAAACAATA	431
DB	1820	CTACTCAACCCAGCGTGTCAACAGCCCTTCCATTGAGGAACTTCCACCTTCAACCACTA	1879
QY	432	TTGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTAGCAACCACTTTAG	491
DB	1880	CTGGTCACTTCCGACCCGAGAGCGAGTCGGCGGAACTGTCAACCAAGCCCACTTTGC	1939
QY	492	AGCTTGGGAAACTTAGGATGATATGCGGAAATGATCAAGTCCGCTTACTGTAGA	551
DB	1940	AGCATGGAAGCACTTGGACTTGAATGGGCCTTATTAATATATGATTGTGTCCACGA	1999
QY	552	AGGCTATCAAAAGTACGCGAAGTGCTA	577
DB	2000	AGGCTACGAGAGTGGCTCTAGTA	2025

RESULT 14

US-10-213-990-64
; Sequence 64, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 712
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-64

Query Match 15.8%; Score 104.8; DB 14; Length 712;

Best Local Similarity 55.8%; Pred. No. 5.2e-20;

Matches 221; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

QY	189	TGTTAATGTCATTAATACTACGAGCCAACTTCCAAACCAATGGTAATGCGTATTATG	248
DB	304	TGGATTCAGAGCGGTCACTACAGCGGCTCTGGAGACCGGAAACGGCTACTCTC	363
QY	249	CGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATATATGTCGACAGTTGGGGCAA	308
DB	364	CGTGTACGGCTGAGACGACGAGTCCGCTGTGCAATCTTACATCGTGGAGAGTTACGCTC	423
QY	309	CTGGCGTCCACCA---GGAGCAACGCTTAAGGGGACCATCATCTGTTGATGGAGGACATA	365
DB	424	CTATGACCCCTCCAGCGGAGCCACCATCTCGGACCGTCGAGAGCGCGGGCCACGTA	483
QY	366	TGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATGCGCACTTTAA	425
DB	484	CAACCTCTACAAGACGACCGGACGAAATCGCGGCTCCATCCAGGGACCGCTACTTTGA	543
QY	426	ACAATATGCGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTAGCAACCA	485
DB	544	CCAGTACTGTCGGTTCGGACTTCGCACCGGACAGTGGAACTGTGACGAGGAACCA	603
QY	486	CTTTAGAGCGTGGGAAACTTAGGATGAATATGGGAAATATGATGAAGTCCGCTTAC	545
DB	604	CTTTGATGCTGGAGAAATCGCGGCTCTGCAATTTGGGAACTTTTACTATATGATTGTC	663
QY	546	TGTAGAGGCTATCAAGTAGCGGAAGTCTAATGT	581
DB	664	GACGGAGGGGTACCGAGAGCGGCTCTGCTACTAT	699

RESULT 15

US-10-213-990-65
; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65

; LENGTH: 666
 ; TYPE: DNA
 ; ORGANISM: Aspergillus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) ... (666)
 US-10-213-990-65

Query Match 15.6%; Score 103.6; DB 14; Length 666;
 Best Local Similarity 56.3%; Pred. No. 1.1e-19;
 Matches 215; Conservative 0; Mismatches 164; Indels 3; Gaps 1;

Qy	203	TAAACTACGGAGCCAACTTCCAAACAAATGGTAATGCGTATTATGCGGTCTATGTTGGA	262
Db	272	TCACCTACAGCGGCTCCTGGCAGACACGCGGAACGGCTACCTCTCCGTGACGGCTGGA	331
Qy	263	CTGTTGACCCCTTTGTCGAATATTATATGTCACAGTTGGGGCAACTGGCGTCCACCA-	321
Db	332	CGACCAGTCCGCTGGTTCGAATTTCTACATCGTGGAGATTACGGCTCTATGACCCCTCCA	391
Qy	322	--GGAGCAACGCTAAGGGACCATCACTGTTGATGGAGGACATATGATATCTACGAGA	379
Db	392	CGGGAGCCACCCATCTCGGCACCGTCGAGAGCGGGGCCACGTACAACTCTACAAGA	451
Qy	380	CTCTTAGAGTCAATCAACCCCTCCATTAAAGGGGATTGCCACATTTAAACAATATTGGAGTG	439
Db	452	CGACCGGACGAAATGCGCGTCCATCCAGGGCACGGCTACTTTGACCAGTACTGGTCGG	511
Qy	440	TTGGAAGATCGAAACGACGAGTGGCAGATTTCTGTGACGCAACCACTTTAGAGCGTGGG	499
Db	512	TTGCGACTTCGACCGGCAGAGTGGAACTGTGACGCAAGAACCACTTTGATGCGTGA	571
Qy	500	AAACTTAGGGATGAATATGGGGAATCTATGAAGTCGCGCTTACTGTAGAGGCTATC	559
Db	572	GAAATGCGGGTCTGCAATTTGGGAACCTTTGACTATATGATTGTCGACGGAGGGGTACC	631
Qy	560	AAAGTAGCGGAAGTGTAAATGT	581
Db	632	AGAGCAGCGGCTCTGCTACTAT	653

Search completed: November 11, 2004, 02:08:22
 Job time : 425.895 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 16:24:32 ; Search time 2874.04 Seconds
(without alignments)
8406.125 Million cell updates/sec

Title: US-09-909-207-1
Perfect score: 663
Sequence: 1 CAATTCGTCACCGACAATTC.....TAACTTGGATAAAACAAT 663

Scoring table: IDENTITY NUC
.Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb.est1:*
2: gb.est2:*
3: gb.htc:*
4: gb.est3:*
5: gb.est4:*
6: gb.est5:*
7: gb.est6:*
8: gb.g881:*
9: gb.g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98.6	14.9	618	7	CF472462 RTDS1_9 C
2	93	14.0	728	7	CN132941 OX1_9_D10
3	93	14.0	772	7	CN133022 OX1_9_D10
4	91.8	13.8	744	7	CF867983 trico13xe
5	91.8	13.8	799	6	CB898036 trico13xe
6	86.6	13.1	738	6	CD464145 ETH1_48 B
7	83.4	12.6	921	6	CD458837 Fg08_04E1
8	82.8	12.5	603	8	AQ160513 mgxb0006C
9	82.2	12.4	720	8	AQ447125 mgxb0005C
10	82.2	12.4	670	8	AQ361561 mgxb0004B
11	82.2	12.4	750	8	AQ160254 mgxb0003L
12	81.6	12.3	786	8	AQ325248 mgxb0001M
13	81.4	12.3	583	8	AQ399120 mgxb0001B
14	76.6	11.6	561	8	AQ396475 mgxb00010M
15	76.4	11.5	617	1	AJ638869 AJ638869
16	76.2	11.5	768	7	CF881056 trico083xj
17	76.2	11.5	822	6	CB907827 trico083xj
18	74.6	11.3	753	8	AQ448084 mgxb00016B
19	74.4	11.2	418	8	AQ398756 mgxb0005L
20	71.8	10.8	746	6	CB901964 trico028xi
21	71.8	10.8	746	7	CF871731 trico028xi
22	69.8	10.5	520	5	BQ165950 WHE0821-0
23	66.2	10.0	561	5	BQ471960 HV04A02r
24	63.2	9.5	473	6	CD464005 ETH1_48_B

C	25	60.4	9.1	483	5	BQ664593	BQ664593 HV04A02u
C	26	53.6	8.1	646	8	AQ449078	AQ449078 mgxb0022H
C	27	51.6	7.8	493	7	CO135442	CO135442 EST830113
C	28	49.4	7.5	490	2	BF200865	BF200865 WHE0821-0
C	29	49.4	7.5	532	4	BM134812	BM134812 WHE0452_F
C	30	48.4	7.3	532	7	CN008236	CN008236 WHE2638_H
C	31	47.8	7.2	743	7	CF865758	CF865758 trico003xb
C	32	47.8	7.2	802	6	CB895680	CB895680 trico003xb
C	33	46.6	7.0	503	5	BQ166480	BQ166480 WHE0861_D
C	34	46.6	7.0	1582	9	CC820765	CC820765 SSH_RfFD1
C	35	46.4	7.0	456	1	AJ637947	AJ637947 AJ637947
C	36	45.2	6.8	587	6	CD033274	CD033274 mgmt012xd
C	37	44.8	6.8	614	6	CA278095	CA278095 SCBPSD203
C	38	41.6	6.3	488	4	BM135798	BM135798 WHE2624_C
C	39	40.4	6.1	386	7	CN470894	CN470894 hh_AB_Bra
C	40	40.2	6.1	665	2	BB664921	BB664921 BB664921
C	41	40.2	6.1	1319	3	AK053390	AK053390 Mus muscu
C	42	39.8	6.0	363	6	CD113872	CD113872 ME1-0031T
C	43	39.6	6.0	704	5	BQ110128	BQ110128 VD0103B07
C	44	38.8	5.9	588	8	AQ630020	AQ630020 RFC1-11-4
C	45	38.8	5.9	750	6	CA447770	CA447770 UI-H-E10-

ALIGNMENTS

RESULT 1
CF472462
LOCUS
DEFINITION
RTDS1_9_C03.g1_A015 Drought-stressed loblolly pine roots DS1 Pinus taeda cDNA clone RTDS1_9_C03_A015 5', mRNA sequence.
CF472462
CF472462.1 GI:34489834
EST.
Pinus taeda (loblolly pine)
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 618)
Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.M., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.
An EST database from drought-stressed loblolly pine (Pinus taeda) roots
JOURNAL
COMMENT
Unpublished (2003)
Other_ESTs: RTDS1_9_C03.b1_A015
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@cuga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES
source

1..618
Location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTDS1_9_C03_A015"
/lab_host="DH10B-T1-phage-resistant E. coli"
/clone_lib="Drought-stressed loblolly pine roots DS1"
/notes="Vector: pSL180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from drought-stressed loblolly pine (Pinus taeda) roots. Water was withheld from

ramet clones until predawn needle water potential reached -1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

```

Query Match      14.9%; Score 98.6; DB 7; Length 618;
Best Local Similarity 57.4%; Pred. No. 4.8e-17;
Matches 198; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 182 AACAGTTGGTAACATGTCCATAACTACGGAGCCCACTTCCAAACCAATGGTAATGGT 241
DB 254 ATCCAGGTAGTGGCAGACATCACTTCTCGGTACCTTACGCCAGCAGAAAGCCT 313
QY 242 ATTTATGCGTCTATGGTGTGAGTGTGACCTCTTGTGCGAATATATATATGTCAGAGTT 301
DB 314 ATCTTGGCGTCTACGGCTGGACCAAGCCCTCTGATCGAATACTACATTTCTCGAAAGCT 373
QY 302 GGGCAACTGGCGTCC---ACCAGAGCAACGCCCTCGATCGCCATATGGGACCATCACTGTTGATGGAG 358
DB 374 ATGGGACCTCAACACCTCGATCCAGCATGACCCATATGGGCACTGTCAACGAGCGAGGTG 433
QY 359 GAACATATGATCTATACGAGACTCTTAGAGTCAATCAACCTCTCCATTAAAGGGGATTGCCA 418
DB 434 CGACCTATGATCTATGAGCACCAGCAAGTCAACAGCCCTCTATCTCGCGCAGCGGA 493
QY 419 CATTAAACATATTTGGAGTGTGGAAGATCGAAACGACGAGTGGCAGCATTTCTGTCA 478
DB 494 CTTTCAACCAATCTATGTTCCATCCGTCAGAGCAAGCGGTCCAGCGGAATGTCACTACAG 553
QY 479 GCAACCACTTTAGAGCGTGGGAAACTTAGGATGAATATGGGA 523
DB 554 CGAACCAITTTCAACGCTGGGTGCTGCTTGGGCGATGAACCTGGGA 598

```

RESULT 2

```

CN132941
LOCUS OX1_9_D10_b1_A002 Oxidatively-stressed leaves and roots Sorghum
DEFINITION bicolor cDNA clone OX1_9_D10_A002 3', mRNA sequence.
ACCESSION CN132941
VERSION CN132941.1 GI:45963408
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 728)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R., Lim, S., Eastman, A., and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)
Other ESTs: OX1_9_D10_g1_A002
Contact: Cordonnier-Pratt, M.M.
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug3-14 (TACTCTAGGGCGCGGACCC)
POLYA=Yes.
Location/Qualifiers

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FEATURES

source

```

1..728
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="Btx623"
/db_xref="taxon:4558"
/clones="OX1_9_D10_A002"
/lab host="DH10B-T1 phage-resistant E. coli"
/clone lib="Oxidatively-stressed leaves and roots"
/notes="Organ: Leaf and Root; Vector: pME18S-FL3; Site: 1:
XhoI; Site 2: XhoI; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 uM methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all
tissue pooled. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites of the
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
insert."

```

ORIGIN

```

Query Match      14.0%; Score 93; DB 7; Length 728;
Best Local Similarity 53.9%; Pred. No. 2e-15;
Matches 214; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

QY 200 CCATAACTAGGAGCCCACTTCCAAACCAATGCTAATCGTATTTATGCGTCTATGGTT 259
DB 101 CCATCAACTATGGCGGTTCTTTAGCCCTCAGGTAACGGCTACTCTGCGTCTACGGCT 160
QY 260 GGACTGTTGACCCCTCTTGTGCAATATATATTTGTCGACAGTTGGGCA---ACTGGCGTC 316
DB 161 GGACTCGCAGCCCTCTGTTGAGTACTACGTACGAGAACTACGGCACTTACAACCTG 220
QY 317 CACCAGGAGCAACGCCCTAAGGGACCATCACTGTTGATGAGGAGCAATATGATATCTACG 376
DB 221 GCTCTGTGGCCAGCAAGGGCACCGCTCTACAACGAGCGGACACCTTACATCTCTACC 280
QY 377 AGACTCTTAGAGTCAATCAACCCCTCCATTAGGGGATTGCCACATTTAAACAATATGGA 436
DB 281 AGACACCCGCTACAACAGCCCTCTTATCGAGGCCACAGACCTTCACAGTACTGGG 340
QY 437 GTGTTGGAAGATCGAAACGACGAGTGGCAGATTTCTGTGACGAACCACTTTAGAGCGT 496
DB 341 CCATCCGCGCAACAAGCGCAGCAGCGCGCGTCAACATCGACACTATCTTCAATGCTT 400
QY 497 GGGAAAATTTAGGATGAATATGGGAAATGTATGAAGTCGCGCTTACTGTAGAAGCT 556
DB 401 GGGCTAAGCGTGTATGAGACTTGGAAACCACTACTACTACAGATCTTGCTACCGAGGAT 460
QY 557 ATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATAC 593
DB 461 ACCAGACAGTGGATCTTCTTCTATCTATGTCCAGAC 497

```

RESULT 3

```

CN133022
LOCUS OX1_9_D10_g1_A002 Oxidatively-stressed leaves and roots Sorghum
DEFINITION bicolor cDNA clone OX1_9_D10_A002 5', mRNA sequence.
ACCESSION CN133022
VERSION CN133022.1 GI:45963542
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 772)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R., Lim, S., Eastman, A., and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)

```


COMMENT

Other ESTs: OX1.9.D10.b1.A002
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmprat@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.
 Seq primer: Sug5 (CTTGTGCTTAAAGTGGC).

FEATURES

Source

1..772

Location/Qualifiers

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="BTx623"

/db_xref="taxon:4558"

/clone="OX1.9.D10.A002"

/lab_host="DH10B-Ti phage-resistant E. coli"

/clone_lib="Oxidatively-stressed leaves and roots"

/notes="Organ: Leaf and Root; Vector: pME18S-FL3; Site 1:

XhoI; Site 2: XhoI; The library was prepared from polyA+

RNA from oxidatively stressed, hydroponically grown

sorghum seedlings. At 8 days of age, growth medium was

supplemented with hydrogen peroxide to 0.003% and leaves

were harvested with 10 uM methyl viologen. Leaves and roots

were harvested at 3, 12 and 27 hr after treatment and all

tissue pooled. Double-stranded cDNA was cloned

unidirectionally into different DraIII sites of the

pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,

3-prime DraIII site is CACCATGTG). XhoI excises the cDNA

insert."

ORIGIN

Query Match 14.0%; Score 93; DB 7; Length 772;
 Best Local Similarity 53.9%; Pred. No. 2e-15;
 Matches 214; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

QY 200 CCATAAATACGAGGACCACTTCCAAACCAATGGTATGCGTATTTATGCGTCTATGGTT 259
 |||||
 Db 324 CCATCAACTATGCGGGTTCTTTCAGCCCTCAGGGTAAACGGCTACCTCTGCGTCTACGGCT 383
 |||||

QY 260 GGAAGTGTGACCTCTGTGCGAATATTTATTCGACAGTTGGGCA---ACTGGCGTC 316
 |||||

Db 384 GGAAGTGTGACCTCTGTGCGAATATTTATTCGACAGTTGGGCA---ACTGGCGTC 443
 |||||

QY 317 CACGAGGACCAAGCCCTTACGAGGACCACTACTGTGTGATGGAGGAACATATGATCTACG 376
 |||||

Db 444 GCTCTGCGCCAGCACAAGGCGACCGTCTACAACGAGCGGCGACACTACGACTCTTACC 503
 |||||

QY 377 AGACTCTTGAAGTCAATCAACCTTCATTAAGGGATGCGCATTTAAACAATATGGA 436
 |||||

Db 504 AGACCAACCCCTACAAACAGCCCTCTATCGACGGCCCAACAGACCTTCAACAGTACTGGG 563
 |||||

QY 437 GTGTTGGAAGTCGAACGACGAGTGGCAGCATTTCTGTGTCAGCAACCTTTAGAGCGT 496
 |||||

Db 564 CCATCCCGCCGAACAGCGGACGCGCGCGCTCAACATGCGACATCTTCAATGCTT 623
 |||||

QY 497 GGGAAACCTTAGGCAATATGGGAAATATGATGAAGTTCGCGCTTACTGTAGAGGCT 556
 |||||

Db 624 GGGCTAACGCTGGTATGAGACTTGGAAACCACTACTACCAGATCTCTGGCTACCGAGGAT 683
 |||||

QY 557 ATCAAAGTACGGAGTGTCTAAATGATATATAGCAATAC 593
 |||||

Db 684 ACCAGACAGTGGATCTTCTTCTATCTATCTATGTGCCAGAC 720
 |||||

RESULT 4

CF867983

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

1..744

Location/Qualifiers

/organism="Hypocrea jecorina"

/mol_type="mRNA"

/strain="QM6a"

/db_xref="taxon:51453"

/clone="tricolix09"

/dev_stage="mycelia"

/clone_lib="T.reesei"

2003"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial

culture grown from 24 hrs to 6 days with varying Carbon

and Nitrogen sources and concentrations."

ORIGIN

Query Match 13.8%; Score 91.8; DB 7; Length 744;
 Best Local Similarity 55.0%; Pred. No. 4.5e-15;
 Matches 202; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

QY 193 AACATGTCATAAACTACGAGGCCAACTTCCAAACCAATGGTATGCGTATTTATGCGTC 252
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Db 353 AACAAAGTTCATCAACTTCTCGGGCAGCTACCAACCCCAACGGCAACAGTACCTCTCGGTG 412
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QY 253 TATGTTGGACTGTTGACCTCTTGTGGAATATTTATTCGACAGTTGGGCAACTCGG 312
 |||||

Db 413 TAGCGTGTGTCGCGCAACCCCTGTATGATGCTCGAGAACTTTTGACACCTAC 472
 |||||

QY 313 CGTCCACCA---GGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGAT 369
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Db 473 AACCGTTCACGGCGCCACCAAGCTGGGCGAGGTCACTCCGACGCGCTACGAC 532
 |||||

QY 370 ATCTACGAGACTTTAGAGTCAATCAACCTTCATTAAGGGGATTTGCCACATTTAAACAA 429
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Db 533 ATTTACCGCAGCGCGCGTCAACACCGCTCCATCATCGGCACCGCCACCTTTTACGAG 592
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QY 430 TATTGAGTGTTCGAAGATCGAAACCGACGAGTGGCAGCATTTCTGTGTCAGCAACCACTTT 489
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Db 593 TACTGTGCTGTCGCGCGCAACCCCGCTCGAGCGGCTCCGTCACACGGGAGAACCACTTC 652
 |||||

QY 490 AGAGCGTGGGAAACTTAGGGATGAATATGGGGAATAATGATGAAGTTCGCGCTTACTGTA 549
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Db 653 AACCGTGGGCTCAGCAAGGCTGACGCTCGGAGCGATGATACCAGATTGTTGCCGTG 712
 |||||

QY 550 GAAGGCT 556
 |||||

CF867983 744 bp mRNA linear EST 31-OCT-2003
 tricolix09.b1 T.reesei mycelial culture, Version 6 October 2003
 Hypocrea jecorina cDNA clone tricolix09, mRNA sequence.

CF867983

CF867983.1 GI:38122635

EST

Hypocrea jecorina (anamorph: Trichoderma reesei)

Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocromycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 744)

Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,

Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,

Ward,M. and Dean,R.A.

Characterization of the protein processing and secretion pathways
 in a comprehensive set of expressed sequence tags from Trichoderma
 reesei

FEMS Microbiol. Lett. 230 (2), 275-282 (2004)

Contact: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

Email: ralph.dean@ncsu.edu

Seq primer: Tr-F1 primer.

Location/Qualifiers

1..744

/organism="Hypocrea jecorina"

/mol_type="mRNA"

/strain="QM6a"

/db_xref="taxon:51453"

/clone="tricolix09"

/dev_stage="mycelia"

/clone_lib="T.reesei"

2003"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial

culture grown from 24 hrs to 6 days with varying Carbon

and Nitrogen sources and concentrations."

Db 713 GGAGGT 719

RESULT 5
CB898036 799 bp mRNA linear EST 02-JUL-2003
LOCUS tricol3xe09 T.reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone tricol3xe09, mRNA sequence.
ACCESSION CB898036
VERSION CB898036.1 GI:30112694
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1. (bases 1 to 799)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
MEDLINE 22803314
PUBMED 12788920
COMMENT Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
1. 799
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tricol3xe09"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

FEATURES
source

ORIGIN
Query Match 13.8%; Score 91.8; DB 6; Length 799;
Best Local Similarity 55.0%; Pred. No. 4.5e-15;
Matches 202; Conservative 0; Mismatches 162; Indels 3; Gaps 1;
QY 193 AACATGTCATTAAGTACGAGGACCACTTCCACCAATGGTAATGCGTATTATGCGTC 252
Db 408 AACAAAGGTATCACTCTCGGGGAGCTACAAACCCGACGGAACAGTACTCTCCGTG 467
QY 253 TATGTTGGACGTGTTGACCCCTTGTTCGAATATTATTGTCGACAGTTGGGGCAACTGG 312
Db 468 TACGGCTGTCCCGCAACCCCTGATCGAGTACTACATGTCGAGAACTTTGGCACTAC 527
QY 313 CGTCCACCA--GGAGCAAGCGCTTAAGGGACATCATCTGTTGATGGAGGAACATATGAT 369
Db 528 AACCCGTCACGGGGGCCCAACGAGTGGGCGAGGTCACTCCGACGGGCGGTCTACGAC 587
QY 370 ATCTACGAGCTTTAGAGTCAATCAACCTCATTAAGGGGATGTCACATTTAAACAA 429
Db 588 ATTATCCGACGAGCGCGTCAACGAGCGTCAATCATCGGACCGCCACTTTTACGAG 647
QY 430 TATTTGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTAGCAACCACTTT 489
Db 648 TACTGTGCTCGCGCGCAACACCGCTCGAGCGGCTCGTCAACACGCGGAACCACTTC 707
QY 490 AGAGCGTGGAAACCTTAGGATGAATATGGGAAATGTATGAAGTCGCGCTTACTGTA 549
Db 708 AACCGTGGGCTCAGCAAGGCGCTGACGCTCGGACGATGGATTACAGATTGTTCGCG 767

QY 550 GGAGGCT 556
Db 768 GGAGGCT 774

RESULT 6
CD464145 738 bp mRNA linear EST 04-JUN-2003
LOCUS ETH1_48_B06.g1 A002 Ethylene-treated seedlings Sorghum bicolor cDNA
DEFINITION clone ETH1_48_B06_A002 5', mRNA sequence.
ACCESSION CD464145
VERSION CD464145.1 GI:31385413
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 738)
Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,
Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R.,
Chua Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P.,
Olaseinde, O., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
(ACC)-treated seedlings
Unpublished (2003)
JOURNAL Other_ESTs: ETH1_48_B06.bl_A002
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).
Location/Qualifiers
1. 738
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="Btx623"
/db_xref="taxon:4558"
/clone="ETH1_48_B06_A002"
/lab_host="Ethylene-treated seedlings"
/clone_lib="Ethylene-treated seedlings"
/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
material from both time points was combined prior to RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites of the
pME18S-FL3 vector (5-prime DraIII site is CACTGTGG,
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
insert."

ORIGIN
Query Match 13.1%; Score 86.6; DB 6; Length 738;
Best Local Similarity 53.5%; Pred. No. 1.4e-13;
Matches 204; Conservative 0; Mismatches 174; Indels 3; Gaps 1;
QY 200 CCATTAACCTACGAGCCCACTTCCAAACCAATGGTATGCGTATTATGCGTCTATGTT 259

Db 345 CCATCAAGTACTCTGCTACTTACAACATCAACGAAACAGCTACCTCGCTGTTTACGGAT 404
 QY 260 GGACTGTTGACCCCTTTGTCGAATATATATTGTCGACAGTTGGGGCACTCGCGTCCAC 319
 Db 405 GGACTCAGAACCCCTCTCATCGAGTACTACATCGTTGAGAACTTCGGCACTTCAACCCCT 464
 QY 320 CA--GGACCAACCGCTAAGGGGACCACATCACTGTTGATGGGGAACATATGATATCTAG 376
 Db 465 CTTCCGGCGCCGAGAAGAAGGTGAGTCACTGTTGACGGATCTGTCTACGACATCTAG 524
 QY 377 AGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTCGCCACATTTAAACAATATGGA 436
 Db 525 TCAGCACCCGTTGTCACGCCCCCTCCATTGAGGGTAAACAAGACCTTTTACGACAGTTCTGT 584
 QY 437 GTGTTGGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACCAACCACTTTAGAGCGT 496
 Db 585 CTGTTGCGACGCAACAGCGATCCAGCGGATCCGTCACACCCGTTCTCACTTCCAGGCT 644
 QY 497 GGGAAACTTAGGATGAATATGGGGAATAATGATGAAGTCGCGCTTACTGTAGAGGCT 556
 Db 645 GGAATAATGTGGCCTCAACCTTGGTAAACCAACTATCAGATCCTTGTGTTGAGGCT 704
 QY 557 ATCAAAGTAGCGGAAGTGCTA 577
 Db 705 ACTACAGCTCGGCTCTGCCA 725

RESULT 7
 CD458837 921 bp mRNA linear EST 14-JUN-2004
 LOCUS Fg08_04b10.A Fg08_AAPC_ECORC_Fusarium_graminearum_complex_substrate
 DEFINITION Gibberella zeae cDNA clone Fg08_04b10, mRNA sequence.

ACCESSION CD458837 GI:31373577
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Gibberella zeae

REFERENCE
 AUTHORS Watson, R.J., Heyes, R., Chapados, J., Couroux, P., Harris, D.J., Hattori, J., Lacroix, C., Ouellet, T., Robert, L.S., Singh, J.A., Spratt, D. and Tinker, N.A.

TITLE A cDNA library prepared from *Fusarium graminearum* grown on a complex plant substrate

JOURNAL Unpublished (2003)
 COMMENT Contact: Watson, Robert J.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
 CANADA

FEATURES
 source
 Tel: (613) 759-1655
 Fax: (613) 759-1701
 Email: watsonrj@agr.gc.ca.

Location/Qualifiers
 1..921
 /organism="Gibberella zeae"
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 /clone="Fg08_04b10"
 /tissue_type="Mycelium"
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 /lab_host="E. coli DH10B"
 /clone_lib="Fg08_AAPC_ECORC_Fusarium_graminearum_complex_s
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/notes="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
 XhoI; *Fusarium graminearum* grown on a complex plant
 substrate-- wheat leaves treated to remove most of the low
 molecular weight, water-soluble components."

ORIGIN

Query Match

12.6%; Score 83.4; DB 6; Length 921;

Best Local Similarity 52.4%; Pred. No. 1.2e-12;
 Matches 208; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 200 CCATTAATCTAGGAGCCAACTTCCAAACCAATGTAATGCGTATTTATGCGTCTATGGTT 259
 Db 363 CCATCAATCTAGGAGGTTCCCTTCAACCCCTCAGGGTAACGGATACCTTTGCGTTACGGAT 422
 QY 260 GGACTGTTGACCCCTCTTGTGCAATATATATTGTCGACAGTTGGGGCAACTCGCGTCCAC 319
 Db 423 GGACCCGGTCCCTCGTCGAGTACTAGCTCATCGAGGTTACGGTTCTTCAACCCCG 482
 QY 320 CAGGA---GCAACGGCTAAGGGGACCATCATCTGTTGATGGAGGAACATATGATATCTAG 376
 Db 483 GCAGCCAGGCTCAGCACCGAGGTACCGTCTACACCGCGGTGACACCTACGATCTCTATA 542
 QY 377 AGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTCGCCACATTTAAACAATATGGA 436
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 QY 437 GTGTTGCAAGATCGAAACGACGAGTGGCAGCATTTCTGTAGCAACCACTTTAGAGCGT 496
 Db 603 CCATCGCGCGCAACAGCGTACCAGCGGCTCCGTCAACATGCAGAACCACTTCAATGCTT 662
 QY 497 GGGAAACTTAGGATGAATATGGGAAATGATGTAAGTCGCGCTTACTGTAGAGGCT 556
 Db 663 GGAGATCTGCTGGCATGAACCTCGGAAACCACTACTACCAGATTCTGGCCACTGAGGTT 722
 QY 557 ATCAAAGTAGCGGAAGTGCTAATGATATAGCAATAT 593
 Db 723 ACCAGAGCAGTGGCTCATCTTCTATCTATGTCCAGAC 759

RESULT 8

LOCUS AQ160513/c
 DEFINITION

ACCESSION AQ160513
 VERSION

KEYWORDS
 SOURCE

ORGANISM
 Gibberella zeae

REFERENCE
 AUTHORS

TITLE

JOURNAL

COMMENT

AQ160513 603 bp DNA linear GSS 09-SEP-1998
 mgxb0006C21r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0006C21r, genomic survey sequence.

ACCESSION AQ160513
 VERSION

KEYWORDS
 SOURCE

ORGANISM
 Magnaporthe grisea (anamorph: Pyricularia grisea)

REFERENCE
 AUTHORS Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.

TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

JOURNAL Unpublished (1998)

COMMENT Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293

Seq primer: GGAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 424.

Location/Qualifiers
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 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice Blast BAC Library"
 /notes="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with

Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCTACTATAGG

RESULT 10	ACCESSION	REFERENCE
AQ361561/c	VERSION	AUTHORS
LOCUS	KEYWORDS	
DEFINITION	SOURCE	
	ORGANISM	

AQ361561
AQ361561.1 GT:4211400

GSS.
Monocotyledonous (anemoph. pyricularia grisea)

Magnaporthe grisea (anamorph: *Typharia grisea*),
Magnaporthe grisea
Magnaporthe grisea
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 720)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.

TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
JOURNAL Genome
COMMENT Unpublished (1998)
 Contact: Dean RA
 Clemson University
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: GGAAACAGCTATGACCATG
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 High quality sequence stop: 321.
 Location/Qualifiers
 1. .720
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 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice Blast BAC Library"
 /notes="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."

FEATURES
 source

ORIGIN
 Query Match 12.4%; Score 82.2; DB 8; Length 720;
 Best Local Similarity 54.1%; Pred. No. 2.5e-12;
 Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;
 148 AAAGGTAAAAAATTCATGAAACACAAACACAAACAGTTGGTAACTATGTCCTATAAAC 207
 445 AAAGGAAAAAAGAGAGACTAACACACACACACAAAAA-----CAGCCGCGTCATCAAC 391
 208 TAGGAGCCAACTTCCAAACCAATGGTAATGGTATTTATGCGTCTATGTTGGACTGTT 267
 390 TACTCGGGCAGCTACAGCCNCAGGGCACTCATACCTGGCGCTCTACGCTGGACGCGC 331
 268 GACCTCTTTCGATATTTATTTGTCAGAGTTGGGCACTGGGCTCCACCA---GGA 324
 330 AACCCGCTGATCGAGTACTACGTGGTGGAGAGCTTTGGCAGCTACAAACCGTCTGCGGC 271
 325 GCAACGCTTAAGGGGACCATCATCTGTTGATGGAGAAACATATGATATCTACGAGACTCTT 384
 270 GCCACCAACCGCGGTCTTCACTCCGACGGCAGCAGCTTACGACATCTCTGTCAGCACC 211
 385 AGAGTCAATCAACCTCCATTAAGGGGATTCGCCATTTAAACAATATGGAGTGTTCGA 444
 210 CGCTACAAACAGCCCTCCATCGACGGCACCAGAACCTTTTCAGCAGTTCTGTCGTCGCG 151
 445 AGATCGAAACGACAGTGGCAGCATTTCTGTGAGCAACCACTTTAGAGCGTGGGAAAC 504
 150 CGCAACAAGCGCGCCAGCGGCACCGTCACTTTGCCAACACACAGTCAACGCTTGGCGCAAC 91
 505 TTAGGATGAATATGGGAAATGTATGAAGTTCGCG---CTTACTGTAGAAGGCTATCAA 561
 90 GCCGCGCTCACTTCGCAACACAGTGGAACTACAGATCTTGGCCGTCGAGGGGTACCAAC 31
 562 AGTAGCGGAGTGTCTA 577
 30 AGCAGCGGCTCCGCCA 15

RESULT 11
 AQL60254/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
 source

ORIGIN
 Query Match 12.4%; Score 82.2; DB 8; Length 750;
 Best Local Similarity 54.1%; Pred. No. 2.5e-12;
 Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;
 148 AAAGGTAAAAAATTCATGAAACACAAACACAAACAGTTGGTAACTATGTCCTATAAAC 207
 445 AAAGGAAAAAAGAGAGCTAACACACACACACAAAAA-----CAGCCGCGTCATCAAC 391
 208 TAGGAGCCAACTTCCAAACCAATGGTAATGGTATTTATGCGTCTATGTTGGACTGTT 267
 390 TACTCGGGCAGCTACAGCCNCAGGGCACTCATACCTGGCGCTCTACGCTGGACGCGC 331
 268 GACCTCTTTCGATATTTATTTGTCAGAGTTGGGCACTGGGCTCCACCA---GGA 324
 330 AACCCGCTGATCGAGTACTACGTGGTGGAGAGCTTTGGCAGCTACAAACCGTCTGCGGC 271
 325 GCAACGCTTAAGGGGACCATCATCTGTTGATGGAGAAACATATGATATCTACGAGACTCTT 384
 270 GCCACCAACCGCGGTCTTCACTCCGACGGCAGCAGCTTACGACATCTCTGTCAGCACC 211
 385 AGAGTCAATCAACCTCCATTAAGGGGATTCGCCATTTAAACAATATGGAGTGTTCGA 444
 210 CGCTACAAACAGCCCTCCATCGACGGCACCAGAACCTTTTCAGCAGTTCTGTCGTCGCG 151
 445 AGATCGAAACGACAGTGGCAGCATTTCTGTGAGCAACCACTTTAGAGCGTGGGAAAC 504
 150 CGCAACAAGCGCGCCAGCGGCACCGTCACTTTGCCAACACACAGTCAACGCTTGGCGCAAC 91
 505 TTAGGATGAATATGGGAAATGTATGAAGTTCGCG---CTTACTGTAGAAGGCTATCAA 561
 90 GCCGCGCTCACTTCGCAACACAGTGGAACTACAGATCTTGGCCGTCGAGGGGTACCAAC 31
 562 AGTAGCGGAGTGTCTA 577
 30 AGCAGCGGCTCCGCCA 15

AQ160254 750 bp DNA linear GSS 09-SEP-1998
 mgxb0003L19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0003L19r, genomic survey sequence.
 AQ160254
 AQ160254.1 GI:3557243
 GSS.
 Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 1 (bases 1 to 750)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 Unpublished (1998)
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: GGAAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 344.
 Location/Qualifiers
 1. .750
 /organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
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 /clone="mgxb0003L19r"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice Blast BAC Library"
 /notes="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."

ORIGIN
 Query Match 12.4%; Score 82.2; DB 8; Length 750;
 Best Local Similarity 54.1%; Pred. No. 2.5e-12;
 Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;
 148 AAAGGTAAAAAATTCATGAAACACAAACACAAACAGTTGGTAACTATGTCCTATAAAC 207
 445 AAAGGAAAAAAGAGAGCTAACACACACACACAAAAA-----CAGCCGCGTCATCAAC 391
 208 TAGGAGCCAACTTCCAAACCAATGGTAATGGTATTTATGCGTCTATGTTGGACTGTT 267
 390 TACTCGGGCAGCTACAGCCNCAGGGCACTCATACCTGGCGCTCTACGCTGGACGCGC 331
 268 GACCTCTTTCGATATTTATTTGTCAGAGTTGGGCACTGGGCTCCACCA---GGA 324
 330 AACCCGCTGATCGAGTACTACGTGGTGGAGAGCTTTGGCAGCTACAAACCGTCTGCGGC 271
 325 GCAACGCTTAAGGGGACCATCATCTGTTGATGGAGAAACATATGATATCTACGAGACTCTT 384
 270 GCCACCAACCGCGGTCTTCACTCCGACGGCAGCAGCTTACGACATCTCTGTCAGCACC 211
 385 AGAGTCAATCAACCTCCATTAAGGGGATTCGCCATTTAAACAATATGGAGTGTTCGA 444

blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

Query Match 12.3%; Score 81.4; DB 8; Length 583;
Best Local Similarity 52.8%; Pred. No. 4.1e-12;
Matches 200; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 154 AAAAAATTCATGAACACACACACCAACAGTTGGTAACATGTCATTAACCTACGGA 213
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QY 214 GCCAACTTCCAAACAAATGATGCTATTTATGGTCTATGTTGGACTGTTGACCTT 273
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QY 331 CCTAAGGGACCATCTACTGTTGATGGAGGAACTATGATATCTACGAGACTCTAGATC 390
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QY 391 AATCAACCTCCATTAAGGGATGGCACAATTTAAACAATATTGGAGTGTTCGAAGATCG 450
DB 205 AACGAGCTTCCATCGAGCGGCAACAGACCTTTACGAGTCTTGCTGGTGGCGCGAAC 146
QY 451 AAACGACGAGTGGCAGCATTTCTGTGACCAACCACTTTAGACGCTGGGAAACTTAGGG 510
DB 145 AAGCGCGCAGCGCAGCGTCACTTTGGCCAAACCACTGCAACCGCTGGCGCAACGCGCG 86
QY 511 ATGAATATGGGAAATGT 529
DB 85 CTCAACTCGGCAACCACT 67

RESULT 14

AQ396475/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AQ396475 561 bp DNA linear GSS 06-MAR-1999
mgxb0010M14f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0010M14f, genomic survey sequence.
AQ396475
GSS.
AQ396475.1 GI:4367502
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 561)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 50
High quality sequence stop: 443.
Location/Qualifiers
1. .561

FEATURES
source

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/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 11.6%; Score 76.6; DB 8; Length 561;
Best Local Similarity 53.7%; Pred. No. 9.6e-11;
Matches 204; Conservative 0; Mismatches 170; Indels 6; Gaps 2;

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QY 199 TCATAAACTACGAGGACCAACTTCCAAACCAAAATGGTAATGCGTATTTATTCGCTTATGGT 258
DB 436 --CATCACTACTCGGGCAGCTACAGCCCGGCACTCATACCTGCGCGTCTACGGC 379
QY 259 TGGACTGTTGACCTCTTGTGCAATATATATTTGTCAGAGTTGGGCGCACTGGCGTCCA 318
DB 378 TGGACGCGCAACCGCTGATGAGTACTAGTGTGGAGAGCTTTGGCAGCTACAACCCG 319
QY 319 CCA---GGAGCAACGCTTAAGGGGACCATCATCTGTTGATGGAGGAACATATATATCTAC 375
DB 318 TGTGCGGCGCCACCAACCGCGGCTCTTCACTCGAGCGGCGAGCACTACGACATCTCTG 259
QY 376 GAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTCGCCACATTTAAACAATATGG 435
DB 258 GTCAGCACCCCGCTACAAACGAGCCCTCCATCGAGCGCACCAAGACCTTTTCAGCAGTCTCG 199
QY 436 AGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTACGACCAACCACTTTAGAGCG 495
DB 198 TCGGTGCGCGCAACAAAGCGCGCAGCGCACCGTCACTTTGGCCAAACCAACGCTCAACGCC 139
QY 496 TGGAAACCTTAGGGATGAA 515
DB 138 TGGCGCAACCGCGGCTCAA 119

RESULT 15

AJ638869
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AJ638869 617 bp mRNA linear EST 05-MAY-2004
AJ638869 Mgc Mycosphaerella graminicola cDNA clone mgc12d03f, mRNA
sequence.
AJ638869
AJ638869.1 GI:47031926
EST.
Mycosphaerella graminicola
Mycosphaerella graminicola
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothricomycetes incertae sedis; Mycosphaerellaceae;
Mycosphaerella.
1 (bases 1 to 617)
Keon, J.P.R., Hargreaves, J.A., Antoniw, J.F. and Hammond-Kosack, K.
Analysis of expressed sequence tags from the wheat fungal leaf
blotch pathogen, Mycosphaerella graminicola (anamorph Septoria
tritici)
Fungal Genet. Biol. (2004) In press

COMMENT

Contact: Keon J
Plant Pathogen Interactions Division,
Rothamsted Research,
Harpenden, Herts, UNITED KINGDOM
Tel: +44(0)1582 763133
Fax: +44(0)1582 760981
Email: john.keon@bbsrc.ac.uk
Insert Length: 800 Std Error: 100.00
Seq primer: M13 reverse.
Location/Qualifiers
1. 617
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wheat leaves 21-25 days after infection with
Mycosphaerella graminicola exhibiting abundant hyphal
growth and asexual sporulation"

FEATURES

source

ORIGIN

Query Match	11.5%;	Score 76.4;	DB 1;	Length 617;
Best Local Similarity	55.6%;	Pred. No. 1.1e-10;		
Matches 168;	Conservative 0;	Mismatches 131;	Indels 3;	Gaps 1;

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Db	425	GCTCTGGCGCTCAGAAGAGGGAACCGTCACCCAGCGGGCACCTACGATATCTCTCC	484
QY	377	AGACTCTTAGATCAATCAACCTCCATTAGGGGATTCGCCACATTTAAACAATATTGGA	436
Db	485	AAACCAACCGGTGTCAACCAACGACCCCTCCATTGACGCACGACGACCTTTTCAGCACTTCTGGA	544
QY	437	GTGTTGGAAGATCGAAACGACAGTGGCAGCATTTCTGTACAGCAACCACTTTAGAGCGT	496
Db	545	GGTGGCCAGCAGAAAGCCGCTCGCGGCACCGTGACCATGAGAACCACTTCGACGCTC	604
QY	497	GG 498	
Db	605	GG 606	

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Job time : 2880.04 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 15:57:32 ; Search time 3599.04 Seconds
(without alignments)
9775.823 Million cell updates/sec

Title: US-09-909-207-4
Perfect score: 744
Sequence: 1 ATGACACAAAGAAATTCAC.....TAACCTTGGATAAAACAAT 744

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_btg.*
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4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	744	100.0	744	6 A48225	A48225 Sequence 4
2	744	100.0	744	6 A48226	A48226 Sequence 5
3	744	100.0	744	6 AR193051	AR193051 Sequence
4	744	100.0	744	6 AR193052	AR193052 Sequence 10
5	744	100.0	1513	6 A48231	A48231 Sequence 11
6	744	100.0	1513	6 A48232	A48232 Sequence 11
7	744	100.0	1513	6 AR193055	AR193055 Sequence
8	744	100.0	1513	6 AR193056	AR193056 Sequence 1
9	713.6	95.9	744	6 A68006	A68006 Sequence 1
10	713.6	95.9	744	6 AR163110	AR163110 Sequence 18
11	671.6	90.3	744	6 A45313	A45313 Sequence 18
12	671.6	90.3	744	6 AR117325	AR117325 Sequence 1
13	663	89.1	663	6 A48222	A48222 Sequence 2
14	663	89.1	663	6 A48223	A48223 Sequence 2
15	663	89.1	663	6 AR193049	AR193049 Sequence
16	663	89.1	663	6 AR193050	AR193050 Sequence
17	587.2	78.9	744	6 A68016	A68016 Sequence 11
18	587.2	78.9	744	6 AR163117	AR163117 Sequence
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20	355.2	47.7	1531	1 BSXNY	XS9059 Bacillus sp
21	281.8	37.9	1454	1 CLOXVNB	M31726 Clostridium
22	279.2	37.5	1070	1 BPXYNA	X00660 Bacillus pu
23	278.2	37.4	4128	1 AF047761	AF047761 Clostridi
24	277.6	37.3	687	1 AY526092	AY526092 Bacillus
25	276.6	37.2	5774	1 AB010958	AB010958 Clostridi
26	275	37.0	3493	1 CST508403	AF508403 Clostridi
27	274.4	36.9	684	1 AF220528	AF220528 Bacillus
28	274.4	36.9	1011	1 AF490981	AF490981 Bacillus
29	273	36.7	1022	6 A42251	A42251 Sequence 1
30	273	36.7	1022	6 A42285	A42285 Sequence 35
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36	273	36.7	1022	6 AR221336	AR221336 Sequence
37	272.8	36.7	681	6 A42280	A42280 Sequence 30
38	272.8	36.7	681	6 A42282	A42282 Sequence 32
39	272.8	36.7	681	6 AR127045	AR127045 Sequence
40	272.8	36.7	681	6 AR127046	AR127046 Sequence
41	272.8	36.7	681	6 AR220049	AR220049 Sequence
42	272.8	36.7	681	6 AR220050	AR220050 Sequence
43	272.8	36.7	681	6 AR221332	AR221332 Sequence
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ALIGNMENTS

RESULT 1	A48225	Sequence 4 from Patent EP0698667-A	744 bp	DNA	linear	PAT 07-MAR-1997
LOCUS	A48225	Sequence 4 from Patent EP0698667-A				
DEFINITION	A48225	Sequence 4 from Patent EP0698667-A				
ACCESSION	A48225	Sequence 4 from Patent EP0698667-A				
VERSION	A48225.1	GI:2302072				
KEYWORDS	unidentified					
SOURCE	unidentified					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 744)					
AUTHORS	De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.					
TITLE	Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof					
JOURNAL	Patent: EP 0698667-A 4 28-FEB-1996;					
COMMENT	SOLVAY (BE)					
	Other publication BE 1008751 960702					
	Other publication BE 1008570 960604					
	Other publication BR 9503454 960305					
	Other publication JP 8092284 960409					
	Other publication FI 953578 960127					
	Other publication CA 2154628 960127					
	Other publication AU 2508695 960208.					

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Best Local Similarity	100.0%; Pred. No. 1.9e-187;
Matches 744; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Db	1 ATGAGCAAAAGAAATGACGTTGATTTAGCCCTTTTGTAGTTTGTGACCTTA 60
Qy	61 CCTGCGAATATTTCCAGGCAAAATTCGTCACCAATTCCTTCGCAACACGATGCC 120
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RESULT 2
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LOCUS Sequence 5 from Patent EP0698667.
DEFINITION A48226
ACCESSION A48226
VERSION A48226.1 GI:2302073
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1. (bases 1 to 744)
AUTHORS De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof
JOURNAL Patent: EP 0698667-A 5 28-FEB-1996;
SOLVAY (BE)
COMMENT Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8052284 960409
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508695 960208.
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ORIGIN
Query Match 100.0%; Score 744; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.9e-187;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCAAAAGAAATTTGACGTTGATTTTGTAGCTTTTGTGTTTGTGCACTAACCTTA 60
Db 1 ATGAGCAAAAGAAATTTGACGTTGATTTTGTAGCTTTTGTGTTTGTGCACTAACCTTA 60
QY 61 CCTGCAGAAATAATTCAGGCACAAATTCGTCCACGACAAATTCATTTGGCAACCGATGGC 120
Db 61 CCTGCAGAAATAATTCAGGCACAAATTCGTCCACGACAAATTCATTTGGCAACCGATGGC 120
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Db 181 GGTACGTTCACTGCCCAATGGAACAATTTTAAACAATATTTATTCGTAAGAGTAAAAA 240
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QY 361 GAATATATATTTGTCAGAGTTGGGCAACTGGGCTCCACGAGGCAACGCTTAAGGGG 420
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QY 421 ACCATCACTGTGTGAGGAGCAATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480
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AR193051	AR193051	Sequence 4 from patent US 6346407.	744 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR193051	Sequence 4 from patent US 6346407.	744 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	AR193051	Sequence 4 from patent US 6346407.	744 bp	DNA	linear	PAT 20-APR-2002
ACCESSION	AR193051	Sequence 4 from patent US 6346407.	744 bp	DNA	linear	PAT 20-APR-2002
VERSION	AR193051.1	GI:20239016				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 744)					
AUTHORS	De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.					
TITLE	Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter					
JOURNAL	Patent: US 6346407-A 4 12-FEB-2002;					
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Db	601	GGGAAATGATGAAGTCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTGCCTAAT	660			
Qy	661	GTATATAGCAATACACTAAGAAATTAACCGTAAACCCCTCTCTCAACTATTAGTAATGACGAG	720			
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Db							721 AGCATAACTTTGGTAAACCAAT 744
RESULT 4							
AR193052							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
Query Match							
Best Local Similarity							
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
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Dd	1	ATGAGACAAAGAATAATTGACGTTCATTTTAGCCCTTTTTAGTTTGTTTGCCTAACCTTA	60				
QY	61	CCTGCAGAAATAATTCAGGCACAATAATCGTCCACCGACAATTCATTTGGCAACACCATGGC	120				
Dd	61	CCTGCAGAAATAATTCAGGCACAATAATCGTCCACCGACAATTCATTTGGCAACACCATGGC	120				
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Dd	121	TATGATTTATGAATTTTCGGAAGATAGCGGTGGCTCTGGGACAAATGATTTCTCAATCATGGC	180				
QY	181	GGTACGTTTCAGTGGCCCAATGGAAACAATGTTTAAACAACATATTTATTCGGTAAAGGTA	240				
Dd	181	GGTACGTTTCAGTGGCCCAATGGAAACAATGTTTAAACAACATATTTATTCGGTAAAGGTA	240				
QY	241	TTCAATGAACACAAAACACCAAACAAGTTGGTAAACATATGTCCTAATAACATAGGAGCC	300				
Dd	241	TTCAATGAACACAAAACACCAAACAAGTTGGTAAACATATGTCCTAATAACATAGGAGCC	300				
QY	301	TTCCAACCAATGTTATGCGTATTTATGCGTCTATGTTGGAGCTGTTGACCCCTCTTGC	360				
Dd	301	TTCCAACCAATGTTATGCGTATTTATGCGTCTATGTTGGAGCTGTTGACCCCTCTTGC	360				
QY	361	GAATATTATATTTGTCGACAGTTGGGGCAACTGGCGTCCACGAGGACCAACGCTTAAGGG	420				
Dd	361	GAATATTATATTTGTCGACAGTTGGGGCAACTGGCGTCCACGAGGACCAACGCTTAAGGG	420				
QY	421	ACCATCACTGTTGATGAGGAAACATATGATATCTATCGAGACTCTTAGAGTCAATCAACCC	480				
Dd	421	ACCATCACTGTTGATGAGGAAACATATGATATCTATCGAGACTCTTAGAGTCAATCAACCC	480				
QY	481	TCCATTAAAGGGATGTCACATTTTAAACAATTTGGAGTGTTCGAAGATCGAAACGCACG	540				
Dd	481	TCCATTAAAGGGATGTCACATTTTAAACAATTTGGAGTGTTCGAAGATCGAAACGCACG	540				
QY	541	AGTGGCACGATTTCTGTGACCAACCACTTTTAGCGGTGGGAAAACTTTAGGGATGAATATG	600				
Dd	541	AGTGGCACGATTTCTGTGACCAACCACTTTTAGCGGTGGGAAAACTTTAGGGATGAATATG	600				
QY	601	GGGAAATGATGAAAGTCGCCCTTATCTGTAGAGGCTATCAAAGTACGCGAAGTCTAAT	660				
Dd	601	GGGAAATGATGAAAGTCGCCCTTATCTGTAGAGGCTATCAAAGTACGCGAAGTCTAAT	660				

Db	1040	ACCATCACTGTTTGATGGAGGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCC	1099
QY	481	TCCATTAAAGGGGATTCGCACATTTAAACAATATTGGAGTGTTCGAAGATTCGAAACGCACG	540
Db	1100	TCCATTAAAGGGGATTCGCACATTTAAACAATATTGGAGTGTTCGAAGATTCGAAACGCACG	1159
QY	541	AGTGGCAGCATTTCTCTCAGCAACCACTTTAGAGCGTGGAAAACTTTAGGGATGAATATG	600
Db	1160	AGTGGCAGCATTTCTCTCAGCAACCACTTTAGAGCGTGGAAAACTTTAGGGATGAATATG	1219
QY	601	GGGAAATGTATGAAGTCGCGCTTACTGTAGAGGCTATCAAGATAGCGGAAGTGTCTAAT	660
Db	1220	GGGAAATGTATGAAGTCGCGCTTACTGTAGAGGCTATCAAGATAGCGGAAGTGTCTAAT	1279
QY	661	GTATATAGCAATACACTAAGAATTTAACGGTAACCCCTCTCTCAACTATTAGTAATGACGAG	720
Db	1280	GTATATAGCAATACACTAAGAATTTAACGGTAACCCCTCTCTCAACTATTAGTAATGACGAG	1339
QY	721	AGCATAACTTTGGATAAAAACAAAT	744
Db	1340	AGCATAACTTTGGATAAAAACAAAT	1363
RESULT 6			
A48232			
LOCUS	A48232	1513 bp	DNA
DEFINITION	Sequence 11 from Patent EP0698667.		
ACCESSION	A48232		
VERSION	A48232.1	GI:2302079	
KEYWORDS	unidentified		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1513)		
AUTHORS	De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.		
TITLE	Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof		
JOURNAL	Patent: EP 0698667-A 11 28-FEB-1996;		
COMMENT	SOLVAY (BE)		
	Other publication BE 1008751 960702		
	Other publication BE 1008570 960604		
	Other publication BR 9503454 960305		
	Other publication JP 8092284 960409		
	Other publication FI 953578 960127		
	Other publication CA 2154628 960127		
	Other publication AU 2508695 960208.		
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ORIGIN			
Query Match	100.0%;	Score 744;	DB 6; Length 1513;
Best Local Similarity	100.0%;	Pred. No. 1.8e-187;	
Matches 744;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	ATGAGACAAAGAAATTGACGTGTGATTTTATAGCCCTTTTATAGTTTGTGTTCGCACTAACCTTTA	60
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Matches	744;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	ATGAGACAAAGAAATTGACGTTGATTTTAGCCTTTTGTAGTTGTTGTTGACCTAAACCTTA	60						
Db	620	ATGAGACAAAGAAATTGACGTTGATTTTAGCCTTTTGTAGTTGTTGTTGACCTAAACCTTA	679						
Qy	61	CCTGCAGAAATTAATTCAGGCACAAATTCGCACCGACAAATTCATTTGGCAACACGATGGC	120						
Db	680	CCTGCAGAAATTAATTCAGGCACAAATTCGCACCGACAAATTCATTTGGCAACACGATGGC	739						
Qy	121	TATGATTAATGAATTTTGGAAAGATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGGC	180						
Db	740	TATGATTAATGAATTTTGGAAAGATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGGC	799						
Qy	181	GGTACGTTTCAGTCCCAATTCGGAACATGTTTAAACAATATTTTCCGTAAGAGTAAAAAA	240						
Db	800	GGTACGTTTCAGTCCCAATTCGGAACATGTTTAAACAATATTTTCCGTAAGAGTAAAAAA	859						
Qy	241	TTCAATGAAACACAAACACACCAACCAAGTTGGTAAACATGTCCTTAATACTACGGAGCCAAC	300						
Db	860	TTCAATGAAACACAAACACACCAACCAAGTTGGTAAACATGTCCTTAATACTACGGAGCCAAC	919						
Qy	301	TTCAACCAAAATGGTAAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCTCTTTGTC	360						
Db	920	TTCAACCAAAATGGTAAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCTCTTTGTC	979						
Qy	361	GAATATTTATATTGTCGACAGTTGGGGCAACTGGCGTCCACAGAGCAACGCCTTAAGGGG	420						
Db	980	GAATATTTATATTGTCGACAGTTGGGGCAACTGGCGTCCACAGAGCAACGCCTTAAGGGG	1039						
Qy	421	ACCATCACTGTTGATGGAGGAAACATATGATATCTACGAGACTCTTAGAGTCATCAACCC	480						
Db	1040	ACCATCACTGTTGATGGAGGAAACATATGATATCTACGAGACTCTTAGAGTCATCAACCC	1099						
Qy	481	TCCATTAAGGGGATTGCCACATTTAAACATATTTGGAGTGTTCGAAGATCGAAACGCACG	540						
Db	1100	TCCATTAAGGGGATTGCCACATTTAAACATATTTGGAGTGTTCGAAGATCGAAACGCACG	1159						
Qy	541	AGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAACTTTAGGGATGAATATG	600						
Db	1160	AGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAACTTTAGGGATGAATATG	1219						
Qy	601	GGGAAAAATGATGAAGTCGCGCTTACTGTAGAAGGCTATCAAGTAGCGGAAGTGCTAAT	660						
Db	1220	GGGAAAAATGATGAAGTCGCGCTTACTGTAGAAGGCTATCAAGTAGCGGAAGTGCTAAT	1279						
Qy	661	GTATATAGCAATACACTAAGAAATTAACGGTTAAACCCCTCTCTCAACTATTAGTAATGACGAG	720						
Db	1280	GTATATAGCAATACACTAAGAAATTAACGGTTAAACCCCTCTCTCAACTATTAGTAATGACGAG	1339						
Qy	721	AGCATAACTTTGGATAAAAACAAAT	744						
Db	1340	AGCATAACTTTGGATAAAAACAAAT	1363						

RESULT 8	AR193056	1513 bp	DNA	linear	PAT 20-APR-2000
LOCUS	AR193056				
DEFINITION	Sequence 11 from patent US 6346407.				
ACCESSION	AR193056				
VERSION	AR193056.1	GI:20239021			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1513)				
TITLE	De Buyl, E., Lahave, A., Ledoux, P. and Detroz, R.				
JOURNAL	xylanase microorganisms producing it, DNA molecules, methods for				
FEATURES	preparing this xylanase and uses of the latter				
source	Patent: US 6346407-A 11 12-FEB-2002;				
	Location/Qualifiers				
	1..1513				
	/organism="unknown"				

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680	DB	CTGCGAAGAAATAAATTCAGGCA	739
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121	QY	TATGATTATGAAATTTTGGAAAGATAGCGGTGGCTCTGGGACAAATGATTTCTCAATCATGGC	180
740	DB	TATGATTATGAAATTTTGGAAAGATAGCGGTGGCTCTGGGACAAATGATTTCTCAATCATGGC	799
181	QY	GGTACGTTTCAGTGGCCCAATGGAA	240
800	DB	GGTACGTTTCAGTGGCCCAATGGAA	859
241	QY	TTCAATTTGAAACACAAACACACAA	300
860	DB	TTCAATTTGAAACACAAACACACAA	919
301	QY	TTCCAAACCAAAATGGTAAATGCGTAT	360
920	DB	TTCCAAACCAAAATGGTAAATGCGTAT	979
361	QY	GAATATTATATCTCGACAGTTGCGGCA	420
980	DB	GAATATTATATCTCGACAGTTGCGGCA	1039
421	QY	ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC	480
1040	DB	ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC	1099
481	QY	TCCATTTAAGGGGATGCCCAATTTAAACATATTTGGAGTGTTCGAAAGATCGAAACGCACG	540
1100	DB	TCCATTTAAGGGGATGCCCAATTTAAACATATTTGGAGTGTTCGAAAGATCGAAACGCACG	1159
541	QY	AGTGGCACGATTTCTGTGACGAAACCACTTTTAGAGCGTGGGAAACCTTTAGGGATGAATG	600
1160	DB	AGTGGCACGATTTCTGTGACGAAACCACTTTTAGAGCGTGGGAAACCTTTAGGGATGAATG	1219
601	QY	GGGAAATATGTAAGTCGCGCTTACTGTGTAAGGCTTATCAAAGTAGCGGAAGTGCTAAT	660
1220	DB	GGGAAATATGTAAGTCGCGCTTACTGTGTAAGGCTTATCAAAGTAGCGGAAGTGCTAAT	1279
661	QY	GTATATAGCAATACACTTAAGAAATTAACCGGTAAACCCCTCTCAACTATTAGTAATGACGAG	720
1280	DB	GTATATAGCAATACACTTAAGAAATTAACCGGTAAACCCCTCTCAACTATTAGTAATGACGAG	1339
721	QY	AGCATAACTTTGGATAAAAAACAAT	744
1340	DB	AGCATAACTTTGGATAAAAAACAAT	1363

RESULT 7					PAT 20-APR-2002
AR193055					
LOCUS			DNA	linear	
DEFINITION	Sequence 10 from patent US 6346407.	1513 bp			
ACCESSION	AR193055				
VERSION	AR193055.1	GI:20239020			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1513)				
TITLE	De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R. Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter				
JOURNAL	Patent: US 6346407-A	10 12-FEB-2002;			
FEATURES	Location/Qualifiers				
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Query Match	100.0%;	Score 744;	DB 6;	Length 1513;	
Best Local Similarity	100.0%;	Pred. No. 1.8e-187;			

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Db

RESULT 10

AR163110

LOCUS

DEFINITION

Sequence 1 from patent US 6270968.

ACCESSION

AR163110

VERSION

AR163110.1 GI:16233600

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

1 (bases 1 to 744)

REFERENCE

Dalb.o slashed.ge.H., Sandal,T., Kauppinen,M.Sakari. and

AUTHORS

Diderichsen,Belashedge.

TITLE

Method of providing a hybrid polypeptide exhibiting an activity of

interest

JOURNAL

Patent: US 6270968-A 1 07-AUG-2001;

FEATURES

Location/Qualifiers

1..744

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 95.9%; Score 713.6; DB 6; Length 744;

Best Local Similarity 97.4%; Pred. No. 2.4e-179;

Matches 725; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 ATGAGCAAAAGAAATGACGTGTTGATTTAGCCCTTTTGTAGTTGTTTGGTCACTAACTTA 60

Db 1 ATGAGCAAAAGAAATGACGTTCATTTTAGCCCTTTTGTAGTTGTTTGGTCACTAACTTA 60

QY 61 CTGCGAATAATATTCAGGCACAAATGCTCAGCGACAAATTCATTCGCAACACGATGC 120

Db 61 CTGCGAATAATATTCAGGCACAAATGCTCAGCGACAAATTCATTCGCAACACGATGC 120

QY 121 TATGATTGAATTTTGGAAAGATAGCGGTGGCTCTGGGCAATGATTCCTCAATCATGCC 180

Db 121 TATGATTGAATTTTGGAAAGATAGCGGTGGCTCTGGGCAATGATTCCTCAATCATGCC 180

QY 181 GGTACGTTCACTGCCCAATGAAATGTTTAAACAATATTTTCCGTAAGGTAAATAA 240

Db 181 GGTACGTTCACTGCCCAATGAAATGTTTAAACAATATTTTCCGTAAGGTAAATAA 240

QY 241 TTCAATGAACACAAACACACCAACCAAGTTGGTAAACATGTCATATACTACGGAGCAAC 300

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QY 361 GAATATTATATGTCGACAGTTGGGCAACTGGGCTCCACGAGGCAACGCTTAAGGGG 420

Db 361 GAATATTATATGTCGACAGTTGGGCAACTGGGCTCCACGAGGCAACGCTTAAGGGG 420

QY 421 ACCATCACTGTTGATGAGGAACAATATGATATCTACGAGACTCTTACAGTCAATCAACCC 480

Db 421 ACCATCACTGTTGATGAGGAACAATATGATATCTATGAACCTCTTACAGTCAATCAACCC 480

QY 481 TCCATTAAGGGGATGTCACATTTAAACAATATTTGAGAGTGTTCGAAGATCGAAACGCAAG 540

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QY 541 AGTGGCAGGATTTCTGTCAGCAACCTTTAGCGGTGGGAAACTTTAGGATGAATATG 600

Db 541 AGTGGCAGGATTTCTGTCAGCAACCTTTAGCGGTGGGAAACTTTAGGATGAATATG 600

QY 601 GGGAAATGATGAAGTCCGCTTACTGTAGAGGCTATCAAAGTACGGAAGTCTAAT 660

Db 601 GGGAAATGATGAAGTCCGCTTACTGTAGAGGCTATCAAAGTACGGAAGTCTAAT 660

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Db 661 GTATATAGCAATACACTAAGAAATTAACGGTAACCCCTCTCTCAACTATTAGTAATGACGAG 720

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Db 721 AGCATAACTCTAGATAAAAAACAAT 744

RESULT 11

A45313

LOCUS

DEFINITION

Sequence 18 from Patent WO9518219.

ACCESSION

A45313

VERSION

A45313.1 GI:2299796

KEYWORDS

SOURCE

unidentified

ORGANISM

unclassified.

1 (bases 1 to 744)

REFERENCE

Van,S.P., Williams,D.P., Iverson,S., Farrell,R.L., Herbes,W.T.,

AUTHORS

Van,D.K., Herweijer,M.A., Van,B.R., Quax,W.J., Goedegebuur,F. and

Jones,B.E.

TITLE

ALKALI-TOLERANT XYLANASES

JOURNAL

Patent: WO 9518219-A 18 06-JUL-1995;

COMMENT

Other publication JP 8507221T 960806

Other publication BR 9405934 951226

Other publication NO 953312 951019

Other publication FI 953920 950821

Other publication AU 1415095 950717.

FEATURES

Location/Qualifiers

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Query Match 90.3%; Score 671.6; DB 6; Length 744;

Best Local Similarity 95.7%; Pred. No. 3.9e-168;

Matches 712; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

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Db 1 ATGAGCAAAAGAAATGACGTGTTGATTTTAGCCCTTTTGTAGTTGTTTGGTCACTAACTTA 60

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Db 61 CCTGCAAGAAATTAATTCAGGCACAAATCGTCACGCAAAATTCATTCGTCACACGATGGC 120

QY 121 TATGATTGAATTTTGGAAAGATAGCGGTGGCTCTGGGCAATGATTCCTCAATCATGCC 180

Db 121 TATGATTGAATTTTGGAAAGATAGCGGTGGCTCTGGGCAATGATTCCTCAATCATGCC 180

QY 181 GGTACGTTCACTGCCCAATGAAATGTTTAAACAATATTTTCCGTAAGGTAAATAA 240

Db 181 GGTACGTTCACTGCCCAATGAAATGTTTAAACAATATTTTCCGTAAGGTAAATAA 240

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Db 718 AGCAATACTTAGATAAAAAACAAT 741

RESULT 12
AR117325 AR117325 744 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 18 from patent US 6140095.
ACCESSION AR117325
VERSION AR117325.1 GI:14098231
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS Williams,D.P., Iverson,S., Farrell,R.Lee., Van Solingen,P.,
Herbes,W.Theresia., Van Der Kleij,W.Antonius.H., Van
Beckhoven,R.Francisus.C., Quax,W.Johannes., Herwijer,M.Adriana.,
Goedegebuur,F. and Jones,B.Edward.
TITLE Alkalitolerant xylanases
JOURNAL Patent: US 6140095-A 18 31-OCT-2000;
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ORIGIN
Query Match 90.3%; Score 671.6; DB 6; Length 744;
Best Local Similarity 95.7%; Pred. No. 3.9e-168;
Matches 712; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

Qy 1 ATGACAAAAGAAATTCAGCTTGATTTTACGCTTTTGTGTTTGTGCTACTAACCTTA 60
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Db 178 GGTCAGTTTCAGTCCCAATGGAACAATGTTTAAACAATATTTATTCGTAAGGTTAAAAA 237
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Db 418 ACCATCACTGTTGATGGAGAACATATGATATCTTAGAGTCAATCAACCC 477
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AR48222 AR48222 663 bp DNA linear PAT 07-MAR-1997
LOCUS Sequence 1 from Patent EP0698667.
ACCESSION AR48222
VERSION AR48222.1 GI:2302069
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 663)
AUTHORS De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof
JOURNAL Patent: EP 0698667-A 1 28-FEB-1996;
COMMENT SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8092284 960409
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508595 960208.
FEATURES Location/Qualifiers
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Query Match 89.1%; Score 663; DB 6; Length 663;
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Best Local Similarity 100.0%; Pred. No. 7.7e-166; Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 202 AACATGTTAAACAACATATTTCCGTAAGGTAAAGAAATTCATGAACACACACAC 261
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QY 262 CAACAAGTTGGTAACATGTCATTAATACTACGAGGCAACTCCCAACAAATGGTAATGG 321
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QY 742 AAT 744
Db 661 AAT 663

RESULT 14

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DEFINITION Sequence 2 from Patent EP0696667.
ACCESSION A48223
VERSION A48223.1 GI:2302070
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 663)
AUTHORS De, B. E., Lahaye, A., Ledoux, P. and Detroz, R.
TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
JOURNAL Patent: EP 0696667-A 28-FEB-1996;
COMMENT SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8092284 960409
Other publication FI 953578 960127

Other publication CA 2154628 960127
Other publication AU 2508695 960208.

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Location/Qualifiers
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ORIGIN

Query Match 89.1%; Score 663; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.7e-166;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CAATCGTCACGACAAATTCATTCGCAACACGATGGCTATGATATGAATTTGGAAA 141
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QY 142 GATAGCGGTGGCTCTGGGCAATGATTCATCATGCGGTACGTTCAAGTCCCAATGG 201
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QY 202 AACATGTTAAACAACATATTTCCGTAAGGTAAAGAAATTCATGAACACACACAC 261
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QY 262 CAACAAGTTGGTAACATGTCATTAATACTACGAGGCAACTCCCAACAAATGGTAATGG 321
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QY 322 TATTTATGCGTCTATGGTTGGACTTTGACCCCTTTGTGCAATATATATTCGACAGT 381
Db 241 TATTTATGCGTCTATGGTTGGACTTTGACCCCTTTGTGCAATATATATTCGACAGT 300

QY 382 TGGGCAACTGGGCTCCACAGGACCAACGCTTAAGGGACCACTCACTGTTGATGGAG 441
Db 301 TGGGCAACTGGGCTCCACAGGACCAACGCTTAAGGGACCACTCACTGTTGATGGAG 360

QY 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGATGGCACA 501
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QY 502 TTTAAACAATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCACGATTTCTGTGACG 561
Db 421 TTTAAACAATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCACGATTTCTGTGACG 480

QY 562 AACCCCTTTAGAGCGTGGGAAAATTTAGGATCAATATGGGAAAATGTATGAATGCGG 621
Db 481 AACCCCTTTAGAGCGTGGGAAAATTTAGGATCAATATGGGAAAATGTATGAATGCGG 540

QY 622 CTCTACTGTAGAAGCTATCAAGTAGCGGAAGTGTAAATGTATATAGCAATACATAAGA 681
Db 541 CTCTACTGTAGAAGCTATCAAGTAGCGGAAGTGTAAATGTATATAGCAATACATAAGA 600

QY 682 ATTAACGGTAACCCCTCTCACTATTTAGTAATGACGAGACATACCTTTGGATAAAAAC 741
Db 601 ATTAACGGTAACCCCTCTCACTATTTAGTAATGACGAGACATACCTTTGGATAAAAAC 660

QY 742 AAT 744
Db 661 AAT 663

Db 661 AAT 663

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Job time : 3600.04 secs

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RESULT 15
AR193049 AR193049 663 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6346407.
ACCESSION AR193049
VERSION AR193049.1 GI:20239014
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 663)
De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
TITLE
Xylanase, microorganisms producing it, DNA molecules, methods for
preparing this xylanase and uses of the latter
JOURNAL
Patent: US 6346407-A 1 12-FEB-2002;
FEATURES
Location/Qualifiers
source 1..663
/organism="unknown"
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ORIGIN
Query Match 89.1%; Score 663; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.7e-166;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 CAATCGTCACGACAAATTCATTTGGCAACCAACGATGCTATGATTGAAATTTGGAAA 141
Db 1 CAATCGTCACGACAAATTCATTTGGCAACCAACGATGCTATGATTGAAATTTGGAAA 60
QY 142 GATAGCGTGGCTCTGGGACAAATGATCTCAATCATGGCGGTACGTTCAAGTGCCTCAATGG 201
Db 61 GATAGCGTGGCTCTGGGACAAATGATCTCAATCATGGCGGTACGTTCAAGTGCCTCAATGG 120
QY 202 AACAAATGTAACAACATATTTCCGTAAAGGTAAATAAATTCATGAAACACAAACACAC 261
Db 121 AACAAATGTAACAACATATTTCCGTAAAGGTAAATAAATTCATGAAACACAAACACAC 180
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QY 502 TTAAACAATATTTGAGGTGTTTGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGAGC 561
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QY 562 AACCACTTTAGAGCTGGGAAACCTTAGGGATGAATATGGGAAATGTATGAAGTCGCG 621
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QY 622 CTCTAGCTAGAGGCTATCAAGTAGCGGAGTGCCTAATGTATATAGCAATACACTAAGA 681
Db 541 CTCTAGCTAGAGGCTATCAAGTAGCGGAGTGCCTAATGTATATAGCAATACACTAAGA 600
QY 682 ATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAGGACATTAACCTTTGGATAAAAAC 741
Db 601 ATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAGGACATTAACCTTTGGATAAAAAC 660
QY 742 AAT 744
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Total number of hits satisfying chosen parameters: 8269772

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	744	100.0	744	2	AAT16102
2	744	100.0	1513	2	AAT16103
3	713.6	95.9	744	2	AAT13067
4	713.6	95.9	871	2	AAT30255
5	671.6	90.3	744	2	AATQ2878
6	663	89.1	663	2	AAT16101
7	587.2	78.9	747	2	AAT13074
8	393	52.8	1068	12	ADJ34947
9	276.6	37.2	1956	12	ADJ35051
10	274.4	36.9	684	12	ADJ34969
11	273	36.7	1022	2	AAQ80923
12	255.6	34.4	2364	3	AAZ51821
13	212.2	28.5	1190	2	AAT90972
14	204.8	27.5	1244	2	AAT08142
15	177.8	23.9	747	12	ADJ35011
16	154.4	20.8	164	2	AAQ82876
17	151.2	20.3	164	2	AAQ82875
18	143.6	19.3	1695	12	ADJ35101
19	142.6	19.2	1338	12	ADJ35151
20	136.2	18.3	1077	12	ADJ34965
21	130.2	17.5	1065	12	ADJ34999

22	128.4	17.3	1047	12	ADJ34949
23	121.2	16.3	678	12	ADJ34955
24	119.4	16.0	1375	2	AAx90405
25	119.4	16.0	1375	2	AAT64930
26	119	16.0	229	2	AAV15063
27	118.4	15.9	573	2	AAV36098
28	117.8	15.8	1207	2	AAT42374
29	117.6	15.8	1041	12	ADJ34943
30	116.8	15.7	1047	12	ADJ35083
31	115.2	15.5	213	2	AAV15059
32	115.2	15.5	596	3	AAA48219
33	115.2	15.5	596	6	AAAD29410
34	115.2	15.5	596	9	AAAL60925
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36	112	15.1	1074	12	ADJ34983
37	112	15.1	1137	12	ADJ35039
38	111.8	15.0	1273	2	AAQ90388
39	111.4	15.0	636	12	ADJ34981
40	111.4	15.0	942	10	ABQ80366
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ALIGNMENTS

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AAT16102
ID AAT16102 standard; DNA; 744 BP.

AC AAT16102;

DT 16-OCT-2003 (revised)
DT 15-MAY-1996 (first entry)

DE Xylanase precursor gene.

XX Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuffs; baking;
KW ss.

OS Bacillus sp; strain 710/1 (LMG P-14798).

XX Key Location/Qualifiers

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FT mat_peptide 82..744

FT /tag= a

FT /tag= b

FT /EC_number= "3.2.1.8"

XX AU9525086-A.

XX 08-FEB-1996.

XX 19-JUL-1995; 95AU-00025086.

XX 26-JUL-1994; 94BE-00000706.

XX 17-MAY-1995; 95BE-00000448.

XX (SOLV) SOLVAY SA.

XX De Buyl E, Lahaye A, Ledoux P, Detroz R;

XX WPI; 1996-117341/13.

XX P-PSDB; AAR92054.

XX Bacillus derived xylanase active over wide pH range - used in treatment
XX of paper pulp, animal feeds and in bakery goods.
XX Claim 9; Page 54-55; 94pp; English.

CC A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was
CC isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The
CC sequence (AAT16103) for the complete gene including 5' and 3'
CC unrelated sequences was also obtd. The gene may be incorporated into a
CC vector and expressed from either its own promoter or from the Bacillus
CC pumilus PRU B12 promoter (see AAR92054), and used for prodn. of
CC recombinant thermostable xylanase in transformed hosts, pref. Bacillus
CC licheniformis or B. pumilus. The enzyme is useful in the paper-pulp,
CC animal feed and baking industries. (Updated on 16-OCT-2003 to standardise
CC OS field)
XX SQ Sequence 744 BP; 246 A; 144 C; 160 G; 194 T; 0 U; 0 Other;

Query Match 100.0%; Score 744; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.5e-210;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||||

RESULT 2
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ID AAT16103 standard; DNA; 1513 BP.

XX AAT16103;
AC
XX
DT 16-OCT-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
DE Xylanase gene.
XX
KW Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
KW ss.
XX
OS Bacillus sp; strain 710/1 (LMG P-14798).
XX
FH Key Location/Qualifiers
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FT 620..1366
FT sig_peptide /*tag= b
FT 620..600
FT mat_peptide /*tag= c
FT 701..1363
FT /*tag= d
FT /EC number= "3.2.1.8"
FT 1367..1513
FT 3'UTR /*tag= e
XX
XX AU9525086-A.
XX
XX 08-FEB-1996.
XX
XX 19-JUL-1995; 95AU-00025086.
XX
XX 26-JUL-1994; 94BE-00000706.
XX 17-MAY-1995; 95BE-00000448.
XX
XX (SOLV) SOLVAY SA.
XX
XX De Buyl E, Lahaye A, Ledoux P, Detroz R;
XX
XX WPI; 1996-117341/13.
XX P-PSDB; AAR92054.
XX
XX Bacillus derived xylanase active over wide pH range - used in treatment
XX of paper pulp, animal feeds and in bakery goods.
XX
XX Claim 10; Page 59-61; 94pp; English.
XX
XX A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was
XX isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The
XX gene may be incorporated into a vector and expressed in transformed
XX hosts, pref. Bacillus licheniformis or Bacillus pumilus, for prodn. of
XX thermostable mature xylanase (AAR92053). The enzyme is useful in the
XX paper pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX
SQ Sequence 1513 BP; 500 A; 282 C; 271 G; 460 T; 0 U; 0 Other;

Query Match 100.0%; Score 744; DB 2; Length 1513;
Best Local Similarity 100.0%; Pred. No. 2.1e-210;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACAAAAGAAATTCAGCTTGAATTTAGCCCTTTTGTGCTTTTGTGCACTAACCTTA 60
Db |||||||
QY 61 CCTGAGACAAATTAATTCAGGCAAAATCGTCACGCAATTCATTGGCAACACGATGGC 120
Db |||||||
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Db |||||||
QY 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATCTCAATCATGGC 180
Db |||||||
QY 740 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATCTCAATCATGGC 799
Db |||||||

Db 661 GTATATAGCAATACACAAAGAAATTAACGGTAACCCCTCTCAACTATTAGTATGACAAG 720
QY 721 AGCATACTTTGGGATAAAACAAT 744
Db 721 AGCATACTCTAGATAAAACAAT 744

RESULT 4
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ID AAV30255 standard; DNA; 871 BP.
XX
AC AAV30255;
DT 17-OCT-2003 (revised)
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 18-AUG-1998 (first entry)
XX
DE DNA encoding a Bacillus agaradherens xylanolytic enzyme.

XX Xylanolytic enzyme; Bacillus agaradherens NCIMB 40482; breakdown;
KW agricultural waste; alcohol fuel; enzymatic treatment; animal feed;
KW release; free pentose sugar; dissolving pulp; cellulose; bio-bleaching;
KW wood pulp; lignocellulosic material; animal feed additive; ss.
XX
OS Bacillus agaradhaerens.

PH Key Location/Qualifiers
FT CDS 82..747
FT /*tag= a
XX
US5770424-A.
XX
23-JUN-1998.
XX
PF 16-AUG-1996; 96US-00698978.
XX
PR 02-JUL-1993; 93WO-DK000218.
PR 30-NOV-1994; 94US-00343600.
PR 06-JUN-1995; 95US-00470398.
XX
PA (NOVO) NOVO-NORDISK AS.

XX Outtrup H, Bisgard-Frantzen H, Schuelein M, Olsen AA;
PI Jorgensen PL, Dambmann C;
XX
DR WPI: 1998-376805/32.
DR P-PSDB; AAW60362.

XX DNA construct encoding Bacillus agaradherens xylanolytic enzyme - and
PT vectors and Bacillus cells containing these, useful for recombinant
PT production of the enzyme for use in agricultural waste breakdown and
XX lignocellulosic material treatment.

PS Claim 1; Col 11-14; 10pp; English.
XX
XX The present sequence encodes a xylanolytic enzyme of Bacillus
CC agaradherens NCIMB 40482. Xylanolytic enzymes are used for enzymatic
CC breakdown of agricultural wastes for production of alcohol fuels,
CC enzymatic treatment of animal feeds to release free pentose sugars,
CC manufacturing of dissolving pulps yielding cellulose and bio-bleaching of
CC wood pulp. They are also used for treatment of lignocellulosic material
CC e.g. paper and pulp, or as an animal feed additive. (Updated on 25-MAR-
CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
CC (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-OCT-2003 to
CC standardise OS field)

XX Sequence 871 BP; 283 A; 171 C; 179 G; 238 T; 0 U; 0 Other;
XX
XX Query Match 95.9%; Score 713.6; DB 2; Length 871;
XX Best Local Similarity 97.4%; Pred. NO. 1.8e-201;
XX Matches 725; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 ATGAGACAAAGAAATGACCTTGATTTAGCCCTTTTGTAGTTTGTGCACTAACCTTA 60
Db 1 ATGAGACAAAGAAATGACCTTGATTTAGCCCTTTTGTAGTTTGTGCACTAACCTTA 60
QY 61 CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAAATTCCTAATGGCAACCGATGGC 120
Db 61 CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAAATTCCTAATGGCAACCGATGGC 120
QY 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAAATGATTCCTAATCATGGC 180
Db 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAAATGATTCCTAATCATGGC 180
QY 181 GGTACGTTTCAGTCCCAATGGAACAATGTTTAAACAATATTTCCGTAAGGTAAACAAA 240
Db 181 GGTACGTTTCAGTCCCAATGGAACAATGTTTAAACAATATTTCCGTAAGGTAAACAAA 240
QY 241 TTCAATGAAACACAAACACACACCAACCAAGTTGGTAACATGCCATAAACTATGGCGCAAC 300
Db 241 TTCAATGAAACACAAACACACACCAACCAAGTTGGTAACATGCCATAAACTATGGCGCAAC 300
QY 301 TTCCAAACCAATGTAATGCGTATTTATGCGTCTATGCTTGGACTGTTGACCCCTTTGTC 360
Db 301 TTCCAGGCAAAACGAAATGCGTATTTATGCGTCTATGCTTGGACTGTTGACCCCTTTGTC 360
QY 361 GAATATTATTTGCGACAGTTGGGCAACTGGCGTCCACGAGCAACGCCCTAAAGGG 420
Db 361 GAATATTATTTGCGACAGTTGGGCAACTGGCGTCCACGAGCAACGCCCTAAAGGG 420
QY 421 ACCATCACTGTTGATGAGGAACAATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480
Db 421 ACCATCACTGTTGATGAGGAACAATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480
QY 481 TCCATTAAAGGGATTGCCACATTTAAACAATTTTGGAGTGTCCGAGATCGAAACGACG 540
Db 481 TCCATTAAAGGGATTGCCACATTTAAACAATTTTGGAGTGTCCGAGATCGAAACGACG 540
QY 541 AGTGCACAGTTTCTGTGACCAACCACTTTAGACGCTGGGAAACTTAGGATGAATATG 600
Db 541 AGTGCACAAATTTCTGTGACCAACCACTTTAGACGCTGGGAAACTTAGGATGAATATG 600
QY 601 GGGAAATGTATGAAGTCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAAT 660
Db 601 GGGAAATGTATGAAGTCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAAT 660
QY 661 GTATATAGCAATACACTAAGAAATTAACGGTAACCCCTCTCTCAACTATTAGTATGACAAG 720
Db 661 GTATATAGCAATACACTAAGAAATTAACGGTAACCCCTCTCTCAACTATTAGTATGACAAG 720
QY 721 AGCATACTTTGGGATAAAACAAT 744
Db 721 AGCATACTCTAGATAAAACAAT 744

RESULT 5
AAQ92878
ID AAQ92878 standard; DNA; 744 BP.
XX
AC AAQ92878;
XX
DT 16-OCT-2003 (revised)
DT 12-FEB-1996 (first entry)
XX
DE Thermostable alkaline endo-1,4-beta-D-xylanase gene.
XX thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning;
KW polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper; pulp;
KW bleaching; ds.
XX
XX Bacillus sp; 1-43-3 (CBS 672.93).
OS
XX
XX WO9518219-A1.
PN
XX

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PD 06-JUL-1995.
XX
PF 23-DEC-1994; 94WO-BP004312.
XX
PR 24-DEC-1993; 93EP-00203694.
XX
PA (KONN ) GIST-BROCADES NV.
XX
PI Van Solingen P, Williams DP, Iverson S, Farrell RL, Herbes WT;
PI Van der Kleijf WA, Herweijer MA, Van Beckhoven RPMC, Quax WJ;
XX Goedegebuur F, Jones BE;
XX
DR WPI: 1995-246385/32.
DR P-PSDB; AAR76551.
XX
XX Novel xylanase enzyme active at high pH - useful in paper and pulp prodn.
XX processes.
XX
XX Claim 4; Page 42-43; 54pp; English.
XX
XX The sequence encodes an alkaline endo-1,4-beta-D-xylanase (G-type) from
XX Bacillus sp. 1-43-3. Fragments of the sequence (e.g. the internal
XX fragments given in AAQ92876 and AAQ92877) may be amplified by polymerase
XX chain reaction, e.g. using primers with sequences AAQ92866, AAQ92867,
XX AAQ92868 and AAQ92869. The DNA may be cloned in Escherichia coli using a
XX plasmid vector for recombinant xylanase production. The xylanase may be
XX used in the paper and pulp industries, where it produces an increase in
XX ISO brightness of softwood pulp of at least 1.0 over non-enzymatically
XX treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg C.
XX The enzyme may be used in production of paper, board and fluff pulp, and
XX has low cellulase activity. The increased brightness produced using the
XX xylanase allows reduction in the amount of bleaching chemicals used.
XX (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 744 BP; 248 A; 145 C; 159 G; 192 T; 0 U; 0 Other;
XX
XX Query Match 90.3%; Score 671.6; DB 2; Length 744;
XX Best Local Similarity 95.7%; Pred. No. 5.1e-189;
XX Matches 712; Conservative 0; Mismatches 29; Indels 3; Gaps 2;
XX
QY 1 ATGAGACAAAGAAATGACGTTGATTTTACGCTTTTATGCTTTTATGTTTTCACCTTA 60
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ATGAGCCAAAGAAATGACGTTGA--TTAACCTTTTATGTTG-TTTCACCTTAACCTTA 57
QY 61 CCTGCAGAAATTAATTCAGGCACAAATCGTCACGCAATTCGATTCGACACACGATGCG 120
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 58 CCTGCAAGAATAAGTCAGGCACAAATCGTCACGCAATTCGATTCGACACACGATGCG 117
QY 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACATGATTTCTCAATCATGGC 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 118 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACATGATTTCTCAATCATGGC 177
QY 181 GGTACGTTACGTCGCCCAATGGAACAATGTTTAAACAATATTTATCCGTAAAGTAAATAA 240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 178 GGTACGTTACGTCGCCCAATGGAATAATGTTTAAACAATATTTATCCGTAAAGTAAATAA 237
QY 241 TTAATGAACAAACAAACACACCAAGTGGTAAACATGTCCTCAATTAACGAGCCAC 300
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 238 TTCAATGAACAAACAAACACACCAAGTGGTAAACATGTCCTCAATTAACGAGCCAC 297
QY 301 TTCCAAACCAATGTAATGCTATTTATGCTCTATGTTGGACTGTTGACCTCTTGTG 360
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 298 TTCCAGCAACCGTAATGCTATTTATGCTCTATGTTGGACTGTTGACCTCTTGTG 357
QY 361 GAATATTATATTGTCAGTGGGCAACTGCGCTCCACGAGCAACGCTTAAGGGG 420
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 358 GAATATTATATTGTCAGTGGGCAACTGCGCTCCACGAGCAACGCTTAAGGGG 417
QY 421 ACCATCACTGTTGATGAGGAACAATATGATATCTACGAGACTTTAGATCAATCAACC 480
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 418 ACCATCACTGTTGATGAGGAACAATATGATATCTATGAAATCTTTAGATCAATCAACC 477
QY 481 TCCATTAAAGGGGATGCGCACATTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACG 540
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 478 TCCATTAAAGGGGATGCGCACATTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACG 537
QY 541 AGTGCCAGATTTCTGTCTAGCAACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATG 600
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 538 AGTGCCAGATTTCTGTCTAGCAACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATG 597
QY 601 GGGAAATGATATGAAGTCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTTAAT 660
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 598 GGGAAATGATATGAAGTCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTTAAT 657
QY 661 GTATATAGCAATACACTAAGAAATTAACGCTTAACCCCTCTCTCACTATTAGTAAATGACGAG 720
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 658 GTATATAGCAATACACTAAGAAATTAACGGAACCCCTCTCTCACTATTAGTAAATGACGAG 717
QY 721 AGCATAACTTGGTATATAAACAAT 744
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 718 AGCATAACTTAGATAAACAAT 741
XX
XX RESULT 6
XX AAT16101
XX ID AAT16101 standard; DNA; 663 BP.
XX AC
XX AAT16101;
XX
XX DT 16-OCT-2003 (revised)
XX DT 15-MAY-1996 (first entry)
XX
XX DE Xylanase gene.
XX
XX KW Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
XX KW ss.
XX
XX OS Bacillus sp; strain 710/1 (LMG P-14798).
XX
XX FH Key Location/Qualifiers
XX FT mat_peptide 1..663
XX FT /*tag= a
XX FT /EC_number= "3.2.1.8"
XX
XX AU9525086-A.
XX
XX PN
XX
XX PD 08-FEB-1996.
XX
XX PF 19-JUL-1995; 95AU-00025086.
XX
XX PR 26-JUL-1994; 94BB-00000706.
XX PR 17-MAY-1995; 95BE-00000448.
XX
XX (SOLV ) SOLVAY SA.
XX
XX De Buyl E, Lahaye A, Ledoux P, Detroz R;
XX
XX WPI; 1996-117341/13.
XX P-PSDB; AAR92053.
XX
XX Bacillus derived xylanase active over wide pH range - used in treatment
XX of paper pulp, animal feeds and in bakery goods.
XX
XX Claim 30; Page 50-51; 94pp; English.
XX
XX A DNA sequence (AAT16101) coding for a thermostable mature xylanase
XX (AAR92053) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-
XX 14798). Sequences were also obtd. (see AAT16102 and AAT16103) for the
XX xylanase precursor and for the complete gene including 5' and 3'
XX untranslated sequences. DNA coding for the mature enzyme may be
XX incorporated into a vector and expressed from either its own promoter or
XX from the Bacillus pumilus PRL B12 promoter (AAQ73996), and used for
XX prodn. of recombinant xylanase in transformed hosts. pref. Bacillus
XX licheniformis or B. pumilus. The enzyme is useful in the paper-pulp,
XX animal feed and baking industries. (Updated on 16-OCT-2003 to standardise
XX OS field)
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XX SQ Sequence 663 BP; 220 A; 131 C; 146 G; 166 T; 0 U; 0 Other;
Query Match 89.1%; Score 663; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.7e-186; Mismatches 0; Indels 0; Gaps 0;
Matches 663; Conservative 0;

QY 82 CAATTCGTCACCGCAATTCATTTGGCAACACACGATGGCTATGATTAATTAATTTGGAAA 141
DB 1 CAATTCGTCACCGCAATTCATTTGGCAACACACGATGGCTATGATTAATTAATTTGGAAA 60

QY 142 GATACGGTGGCTCTGGGACAAATGATTTCAATCATGGCGGTACGTTCACTGCCAATGG 201
DB 61 GATACGGTGGCTCTGGGACAAATGATTTCAATCATGGCGGTACGTTCACTGCCAATGG 120

QY 202 AACATGTTAAACACATATTTCCGTAAGGTAAATAATTCATGAACACACACACAC 261
DB 121 AACATGTTAAACACATATTTCCGTAAGGTAAATAATTCATGAACACACACACAC 180

QY 262 CAACAAGTTGGTAACATGTCATAACTACGAGGCCAACTTCCAAACCAATGGTAATGCG 321
DB 181 CAACAAGTTGGTAACATGTCATAACTACGAGGCCAACTTCCAAACCAATGGTAATGCG 240

QY 322 TATTTATGGCTATGGTTGACTGTTGACCTCTTGTGCAATATTAATTTGTCGACAGT 381
DB 241 TATTTATGGCTATGGTTGACTGTTGACCTCTTGTGCAATATTAATTTGTCGACAGT 300

QY 382 TGGGCAACTGGCGTCCACGAGGACACGCTTAAGGGGACCATCTGTTGATGGAGGA 441
DB 301 TGGGCAACTGGCGTCCACGAGGACACGCTTAAGGGGACCATCTGTTGATGGAGGA 360

QY 442 ACATATGATATACGAGACTCTTAGAGTCAATCAACCTGATTAAGGGGATGCCACA 501
DB 361 ACATATGATATACGAGACTCTTAGAGTCAATCAACCTGATTAAGGGGATGCCACA 420

QY 502 TTTAAACATATTTGGAGTCTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTCAGC 561
DB 421 TTTAAACATATTTGGAGTCTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTCAGC 480

QY 562 AACCACTTTAGACGCTGGGAAACTTAGGATGAATATATGGGAAATATGATGAAGTCGG 621
DB 481 AACCACTTTAGACGCTGGGAAACTTAGGATGAATATATGGGAAATATGATGAAGTCGG 540

QY 622 CTTACTGTAGAGGCTATCAAGTATGACGAGTGAAGTCTTAATGATATAGCAATACACTAAGA 681
DB 541 CTTACTGTAGAGGCTATCAAGTATGACGAGTGAAGTCTTAATGATATAGCAATACACTAAGA 600

QY 682 ATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAGACATAACTTTGGATATAAAC 741
DB 601 ATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAGACATAACTTTGGATATAAAC 660

QY 742 AAT 744
DB 661 AAT 663

RESULT 7
AAV13074
ID AAV13074 standard; DNA; 747 BP.
AC AAV13074;
XX AAV13074;
DT 19-MAY-1998 (first entry)
XX Xylanase activity positive clone DNA SEQ ID NO:11.
DE Bacillus sp; xylanase; glycosyl hydrolase family 11; isolation;
KW microorganism; identification; hybrid DNA; ss.
XX Synthetic.
OS Bacillus sp.
XX Key Location/Qualifiers
FH

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FT CDS 1..747
FT /*tag= a
FT /product= "positive clone for xylanase activity"
XX WO9743409-A2.
XX 20-NOV-1997.
XX 12-MAY-1997; 97WO-DK000216.
XX 10-MAY-1996; 96DK-00000562.
XX (NOVO ) NOVO-NORDISK AS.
XX Dalboge H, Diderichsen B, Sandal T, Kauppinen S;
XX WPI; 1998-008878/01.
XX Isolating novel DNA sequences from microorganisms - without the need for
XX culturing the microorganism.
XX Example 1; Page 35; 72pp; English.
XX The present sequence represents a positive clone for xylanase activity
XX from an example of the present invention. The present invention describes
XX a novel method for providing a novel DNA sequence encoding a polypeptide
XX from a microorganism with an activity of interest. The method comprises:
XX (i) PCR amplification of the DNA with PCR primers with homology to (a)
XX known gene(s) encoding a polypeptide with an activity of interest; (ii)
XX linking the obtained PCR product of a 5' structural gene sequence and a
XX 3' structural gene sequence; (iii) expressing the resulting hybrid DNA
XX sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide
XX with the activity of interest or a related activity; and (v) isolating
XX the hybrid DNA sequence identified in step (iv). This method provides for
XX identification and isolation of sequences from microorganisms without
XX having to cultivate and isolate the microorganism
XX Sequence 747 BP; 236 A; 168 C; 154 G; 189 T; 0 U; 0 Other;
Query Match 78.9%; Score 587.2; DB 2; Length 747;
Best Local Similarity 86.8%; Pred. No. 6.3e-164;
Matches 646; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 1 ATGAGACAAAAGAAATTTGACGTTGATTTAGCTTTTACCTTTTGTGTTGCACTAACCTTA 60
DB 1 ATGAGACAAAAGAAATTTGACGTTGATTTAGCTTTTACCTTTTGTGTTGCACTAACCTTA 60
QY 61 CCTCAGAAATAATTCAGGCAAAATCGTCACGACAAATTCATTTGGCAACACGATGGC 120
DB 61 CCTCAGAAATAATTCAGGCAAAATCGTCACGACAAATTCATTTGGCAACACGATGGC 120
QY 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAAATGATTCATCATGGC 180
DB 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAAATGATTCATCATGGC 180
QY 181 GGTACGTTCACTGCCCAATGGAACAAATTTAAACACATATTTATTCGTAAGGTAAATAA 240
DB 181 GGTACGTTCACTGCCCAATGGAACAAATTTAAACACATATTTATTCGTAAGGTAAATAA 240
QY 241 TTCAATGAAACACAAACACACCAACCAAGTTGTTAAACATGTCATTAACACTACGAGCCAAC 300
DB 241 TTCAATGAAACACAAACACACCAACCAAGTTGTTAAACATGTCATTAACACTACGAGCCAAC 300
QY 301 TTCCAAACCAATGGTAATGGCTATTTATGCGTCTATGTTGGACTGTTGACCTCTTCTC 360
DB 301 TTCCAAACCAATGGTAATGGCTATTTATGCGTCTATGTTGGACTGTTGACCTCTTCTC 360
QY 361 GAATATTATTTGTCGACATGTTGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGG 420
DB 361 GAATATTATTTGTCGACATGTTGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGG 420
QY 421 ACCATCACTGTTGATGGAGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACC 480

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Db 421 ACCATCACTGTTGACGGGGAGCGTATGATATCTACAAAGCACCAACAGGTCAATCAGCCA 480
QY 481 TCATTAAGGGGATGCGACATTTAAACAATATTCGAGTGTTCGAAGATCGAAACGACG 540
Db 481 TCTATTCAGGGCAGCGCCACCTTCAATCAGTACTGCTGATTCGACAGACGAGCGGACC 540
QY 541 AGTGGCAGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATG 600
Db 541 AGCGGCACGTGCTACACGCGCAACCACTTTAATGCTGGCTGCTCTGGCATGATATG 600
QY 601 GGGAAATGTATGAAGTCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAGTCTTAAT 660
Db 601 GGTGATTCATTTACAGATCCTGTTACTGAGGGCTACCAATCTACCGAGTCTTAAT 660
QY 661 GTATATAGCAATACACTAAGAAATTAACGGTAAACCTCTCTCACTATTAGTAATGACGAG 720
Db 661 GTATATAGCAATACACTAAGAAATTAACGGTAAACCTCTCTCACTATTAGTAATGACGAG 720
QY 721 AGCATAAATTTGGTAATAAAACAAT 744
Db 721 AGCATAAATTTGGTAATAAAACAAT 744

RESULT 8

ADJ34947
ID ADJ34947 standard; DNA; 1068 BP.

XX AC ADJ34947;

XX DT

XX DN

XX DE

XX DE

XX DE DNA encoding xylanase from an environmental sample seq id 163.

XX KW antibacterial; fungicide; thermostable xylanase activity;

XX KW dough conditioning; beverage production; nutritional supplement;

XX KW animal feed; lignin reduction; wood product; xylan; bacterial infection;

XX KW fungal infection; coccidiosis; gene; ds.

XX OS Unidentified.

XX OS

XX OS

XX OS

XX OS

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XX OS

CC This sequence encodes xylanase protein isolated from an environmental sample.

XX Sequence 1068 BP; 303 A; 249 C; 279 G; 237 T; 0 U; 0 Other;

SQ Query Match 52.8%; Score 393; DB 12; Length 1068;

Best Local Similarity 75.2%; Pred. No. 3.9e-106;

Matches 518; Conservative 0; Mismatches 165; Indels 6; Gaps 2;

QY 1 ATGAGACAAAAGAAATGACCTTGAATTTTACCTTTTATGTTTGTGTTGCACTTAACCTTA 60

Db 1 ATGAAAGCAAGAGAAATGAAGTTGTTGCCGCAATTTTCTCTGTTTACGTTGCACTT 60

QY 61 CCTGCAGAAAATAATTCAGGCACAAATCGTCACCGACAATTCATTTGGCAACCAACGATGGC 120

Db 61 CCTGGG---CAGTCCATGCGCAGACGATCACCAGCAATTCGGTCGGTACGATACGGT 117

QY 121 TATGATATGAATTTTGGAAAAGATAGCGGTGGCTCTGGGACAAATGATTTCTCAATCATGGC 180

Db 118 TATGACTATGAATACTGGAAGACAGC---GGGAATGGAACATATGTTTCTCGGTAGTGGC 174

QY 181 GGTAGCTTCAGTCCCAATGGAACAATGTTAAACAATATTTATCCGTAAAGGTAATAAAA 240

Db 175 GGTAGCTTCAGTCCCAATGGAACAATGTTAAACAATATTTATCCGTAAAGGTAATAAAA 234

QY 241 TTCATGAAACACAAACACACCAACAAAGTTGGTAAACATGTCATAAACTACGAGCCCAAC 300

Db 235 TTCATGAAACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 294

QY 301 TTCCAAACCAATGTTAAATGCGGTATTTATGCGTCTATGTTGAGTCTTTGACCTCTTGTG 360

Db 295 TACCAACCAATGTTAAATGCGGTATTTATGCGTCTATGTTGAGTCTTTGACCTCTTGTG 354

QY 361 GAATATTTATGTCGACAGTTGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGG 420

Db 355 GAATATTTATGTCGACAGTTGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGG 414

QY 421 ACCATCACTGTTGATGAGGAAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCC 480

Db 415 ACTGTTAAGCTTGACGAGGAAACGATATGACATTTATGAGCAACTCGTCTCAACGACCT 474

QY 481 TCCATTAAGGGGATTTGCCACATTTAAACAATATTTGAGTGTTCGAAGATCGAAACGACG 540

Db 475 TCCATTAAGGGGATTTGCCACATTTAAACAATATTTGAGTGTTCGAAGATCGAAACGACG 534

QY 541 AGTGGCAGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATG 600

Db 535 AGCGGAACCAATATCTGTAAGCGGACACTTTAAGGCTTGGGAGAAATTTGGGATGACCATG 594

QY 601 GGGAAAATGTATGAAGTCCGCTTACTGTAGAGGCTATCAAAAGTAGCGGAAGTGTCTAAT 660

Db 595 GGCAGATGTATGAAGTCCGCTTACGGTTGAAGGCTATCAAAAGCAGTGGNAGCGCTAAT 654

QY 661 GTATATAGCAATACACTAAGAAATTAACCG 689

Db 655 GTGATATAGCATACTACACTGACGATCGGCGG 683

RESULT 9

ADJ35051

ID ADJ35051 standard; DNA; 1956 BP.

XX AC ADJ35051;

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

22-APR-2004 (first entry)

DNA encoding xylanase from an environmental sample seq id 267.

antibacterial; fungicide; thermostable xylanase activity;

dough conditioning; beverage production; nutritional supplement;

animal feed; lignin reduction; wood product; xylan; bacterial infection;

fungal infection; coccidiosis; gene; ds.

OS Unidentified.
XX WO2003106654-A2.
XX 24-DEC-2003.
XX 16-JUN-2003; 2003WO-US019153.
XX 14-JUN-2002; 2002US-0389299P.
XX (DIVE-) DIVERSA CORP.
XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
PI Esteghlalian A;
XX WPI; 2004-099016/10.
XX P-PSDB; ADJ35052.
XX Novel xylanase recombinant polypeptide useful for improving textile
PT texture, treating paper, eliminating microorganisms.
XX Claim 1; SEQ ID NO 267; 570pp; English.
XX The invention describes an isolated or recombinant polypeptide (I),
CC having 50% or more identity to 190 300-1200 residue amino acid sequences
CC (SI), given in the specification, over a region of 100 or more residues
CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
CC dough conditioning; beverage production; as a nutritional supplement in
CC animal feed; reducing lignin in a wood or a wood product; and for
CC eliminating and protecting animals from a microorganism comprising xylan.
CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
CC acid encoding a polypeptide having a xylanase activity which involves
CC amplification of a template nucleic acid with a primer pair capable of
CC amplifying (II) or its subsequence. (I) is useful for treating and
CC preventing bacterial infection and fungal infection e.g. coccidiosis.
CC This sequence encodes xylanase protein isolated from an environmental
CC sample.
XX Sequence 1956 BP; 614 A; 384 C; 423 G; 535 T; 0 U; 0 Other;
SQ

Query Match 37.2%; Score 276.6; DB 12; Length 1956;
Best Local Similarity 66.2%; Pred. No. 2e-71;
Matches 415; Conservative 0; Mismatches 209; Indels 3; Gaps 1;

QY 69 AATATTTCAGGCACCAATCGTCACCGACAATTCCTATGGCAACACGATGGCTATGATTA 128
DB 81 AGTATCGCGCGGGAATTAATTCAGCAATGAGACAGGCACACATGGAGGTACGACTA 140
QY 129 TGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCATATCATGGCGGTACGTT 188
DB 141 TGAGCTCTGMAAGA---CTACGGAAATACGATTATGGAACCTTAACGACGGTGGTACTTT 197
QY 189 CAGTGGCCCAATGGAACAATGTTAAACAATATATTCCTTAAGGTAAATAAATTCGAATGA 248
DB 198 TAGTTGTCATGAGTAATATCGGTATGACATATTTAGAAAGGGAGAAATTAATTC 257
QY 249 AACACAAACACACCAAGTTGGTAAACATGTCCATAAATACGGAGCAATTCCTCAAC 308
DB 258 CGCAAAACCTATCAGAAATAGGAGATATAGTAGTTGATGGTGTGATTACAATCC 317
QY 309 AATAGTAAATGCTATTTATGGTCTATGGTTGAGCTGTGACCTCTTGTGCAATATTA 368
DB 318 AAACGGAAATTCCTATTTGTGTTTACGGTTTGGACAAGAAATTCACCTGGTTGAATATTA 377
QY 369 TATTTGTCAGATGGGCACTGGCGTCCACCAGAGCAACGCTTAAGGGACCATCAC 428
DB 378 CATTTAGAAAGCTGGGGAGCTGGCGTCCACTGGAGCAACCCCAAGGAAACCATCAC 437
QY 429 TGTGATGGAGGAACATATGATATCTACGAGACTTTAGAGTCAATCAACCCCTCCATTA 488
DB 438 AGTGATGGCGGTATTATGAATATATGAACACTCCCGGTAAATCAGCCCTTCCATCGA 497
QY 489 GGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAGATCGAAACGACAGTGGCAC 548

DB 498 TGGAACTGCGACATTCACAAATATTGGAGTGTTCGTACATCAAGAGAACAAAGCGAAC 557
QY 549 GATTTCTGTGACCAACCACTTTAGAGCGTGGGAAACTTAGGATGAATATGGGGAATAAT 608
DB 558 AATATCTGTCACTGAACATTTAAACAGTGGGAAGAAATGGGCNTGCGAATGGGTAAAT 617
QY 609 GTATGAAGTCGGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTTAATGTATATAG 668
DB 618 GTATGAAGTTCCTTACCGTTGAAGGTTATCAGAGCAGTGGGTACGCTAATGTATATA 677
QY 669 CAATACACTAAGAAATTAACGGTAACCC 695
DB 678 GAATGAATCAGAATAGGTGCAATCC 704

RESULT 10
ADJ34969
ID ADJ34969 standard; DNA; 684 BP.
XX AC ADJ34969;
XX DT 22-APR-2004 (first entry)
XX DE DNA encoding xylanase from an environmental sample seq id 185.
XX KW antibacterial; fungicide; thermostable xylanase activity;
KW dough conditioning; beverage production; nutritional supplement;
KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
KW fungal infection; coccidiosis; gene; ds.
XX OS Unidentified.
XX PN WO2003106654-A2.
XX PD 24-DEC-2003.
XX PF 16-JUN-2003; 2003WO-US019153.
XX PR 14-JUN-2002; 2002US-0389299P.
XX PS (DIVE-) DIVERSA CORP.
XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
PI Esteghlalian A;
XX WPI; 2004-099016/10.
XX P-PSDB; ADJ34970.
XX Novel xylanase recombinant polypeptide useful for improving textile
PT texture, treating paper, eliminating microorganisms.
XX Claim 1; SEQ ID NO 185; 570pp; English.
XX The invention describes an isolated or recombinant polypeptide (I),
CC having 50% or more identity to 190 300-1200 residue amino acid sequences
CC (SI), given in the specification, over a region of 100 or more residues
CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
CC dough conditioning; beverage production; as a nutritional supplement in
CC animal feed; reducing lignin in a wood or a wood product; and for
CC eliminating and protecting animals from a microorganism comprising xylan.
CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
CC acid encoding a polypeptide having a xylanase activity which involves
CC amplification of a template nucleic acid with a primer pair capable of
CC amplifying (II) or its subsequence. (I) is useful for treating and
CC preventing bacterial infection and fungal infection e.g. coccidiosis.
CC This sequence encodes xylanase protein isolated from an environmental
CC sample.
XX Sequence 684 BP; 221 A; 129 C; 158 G; 176 T; 0 U; 0 Other;
SQ

Query Match 36.9%; Score 274.4; DB 12; Length 684;
Best Local Similarity 64.6%; Pred. No. 5.8e-71;

Matches 442; Conservative 0; Mismatches 236; Indels 6; Gaps 2;

QY 1 ATGAGACAAAGAAATGAGTTGATTTTGGCTTTTGTAGCTTTTGTAGTTTGTGCTACCTTA 60
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 Db 1 ATGAATTTGAAAGATGAGGCTGTGTGTGTGATGTGATTTGGATTTGTGCTGACACTG 60
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QY 61 CCTGCAGAAATTAATTCAGGCACAAATCGTCACCGCAATTCATTTGGCAACCAACGATGGC 120
 |||||
 Db 61 ACGGCTGTGCGAGCTCATCGGAACGATTTATGATATATAGATAGGACACACAGCGGA 120
 |||||

QY 121 TATGATTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCTCAATCATGGC 180
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 Db 121 TACGATTTTGAATTTGGAAGATTTACGGAATACCTCG---ATGACACTCAATAACGGC 177
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QY 181 GGTACGTTGAGTCCCAATGGAACAAATGTTTAAACAATATTTTCGTTAAAGTTAAAAA 240
 |||||
 Db 178 GGGGCAATTTAGTGCAGCTGGAACAAATTTGGAATGCTTATTTGGAAGGAAAGAG 237
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QY 241 TTCAATGAACAAACACACCAACAAAGTTGGTAAACATGTCATTAACACTACGGAGCAAC 300
 |||||
 Db 238 TTGATTTCCACTAAACTCATCACTTGGCAACATCTCCATCAACTACACGAGCC 297
 |||||

QY 301 TTCCAAACAAATGTAATGCGTATTATGCGTCTATGTTGAGTGTGACCTCTTGTGC 360
 |||||
 Db 298 TTTAACCCTGGCGGAATTCCTATTATGTTGCTATGGCTGGACACAATCTCCATTAGCT 357
 |||||

QY 361 GAATATATATTTGTCAGAGTTGGGGCAACTGGCTCCACAGGAGCAACGCTTAAGGG 420
 |||||
 Db 358 GAATACTACATTTGTTGAGTTCATGGGGCACATATCGTCCCAACAGG---AACGTATAAGGA 414
 |||||

QY 421 ACCATCACTGTTGATGGAGGAAATATATATCTACGAGACTCTTAGAGTCAATCAACCC 480
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 Db 415 TCATTTTATGCGATGGAGGCAATATGACATATATGAACGCTCGTGTCAATCAGCT 474
 |||||

QY 481 TCATTAAGGGATTCACCATTTAAACAATATTTGAGTGTGTCGAAGATCGAAACGACG 540
 |||||
 Db 475 TCTATCATTTGGAGAGCTACCTTCAACAATATTTGAGTGTAGCTCAACAACAAACGACA 534
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QY 541 AGTGGACAGATTTCTGTGACCAACCACTTTAGAGCTGGGAAACTTAGGGATGATATG 600
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 Db 535 AGCGGAACCTGTTTCCGCTAGTGAGCATTTTAAATAATGGGAAAGCTTAGGCATGCAATG 594
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QY 601 GGGAAATGATGAAGTCCGCTTACTGTAGAAGGCTATCAAGTAGTGGGAAGTGTCTAAT 660
 |||||
 Db 595 GGAATAATGTGAACACAGATTAATCTGTAAGAGGCTACCGAAGCAACGGAAGTGGAT 654
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QY 661 GTATATAGCAATACACTAAGAATT 684
 |||||
 Db 655 GTCATGACGAATCAGCTGATGATT 678
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RESULT 11
 AAQ80923
 ID AAQ80923 standard; DNA; 1022 BP.
 XX AC AAQ80923;
 XX 02-AUG-1995 (first entry)
 XX B. pumilus xylanase gene.
 XX Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping; biobleaching;
 XX bleaching; Bacillus licheniformis; ss.
 XX Bacillus pumilus.
 XX Key Location/Qualifiers
 XX 5'UTR 1..185
 XX /tag= a
 XX /note= "claim 12"
 XX misc_difference 107
 XX /tag= b
 XX /note= "base n at position 107 is not identified in the

FT CDS specification"
 FT 186..869
 FT /*tag= c
 FT sig_peptide 186..266
 FT /*tag= d
 FT /note= "claim 11"
 FT mat_peptide 267..866
 FT /*tag= e
 FT /EC number= "3.2.1.8"
 FT /note= "claim 10"
 XX GB2279955-A.
 XX 18-JAN-1995.
 XX 15-JUL-1993; 93GB-00014780.
 XX 15-JUL-1993; 93GB-00014780.
 XX (SOLV) SOLVAY & CIE.
 XX Amory A, Andre C, De Buyl E, Detroz R, Lahaye A, Ledoux P;
 XX WPI; 1995-039214/06.
 XX P-PSDB; AAR68849.
 XX Purified xylanase from Bacillus pumilus PRL B12 - esp. produced in
 XX transformed Bacillus licheniformis, and related DNA vectors, etc., used
 XX for pre-treatment of wood pulp to reduce chlorine or ozone consumption in
 XX subsequent bleaching.
 XX Claim 13; Fig 1a-1b; 97pp; English.
 XX A Bacillus pumilus PRL B12 (ATCC 55443) gene library was screened for
 XX recombinant plasmids carrying the xylanase gene. A chromosomal fragment
 XX obtained from isolate pBPX1 was subcloned and expressed in Escherichia
 XX coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3AI
 XX fragment) carried by a selected transformant is given in AAQ80923
 XX Sequence 1022 BP; 329 A; 197 C; 229 G; 266 T; 0 U; 1 Other;
 SQ Query Match 36.7%; Score 273; DB 2; Length 1022;
 Best Local Similarity 63.4%; Pred. No. 1.8e-70;
 Matches 452; Conservative 0; Mismatches 255; Indels 6; Gaps 2;
 QY 1 ATGAGACAAAGAAATGAGTTGATTTTGGCTTTTGTAGCTTTTGTGCTACCTTA 60
 |||||
 Db 186 ATGAATTTGAAAGATTTGAGCTGTGTGTGTGATGTGATTTGGATTTGTGCTGACACTG 245
 |||||

QY 61 CCTGCAGAAATTAATTCAGGCACAAATCGTCACCGCAATTCATTTGGCAACCAACGATGGC 120
 |||||
 Db 246 ACGGCTGTGCGGCTCATCGGAACGATTTATGATATAGGATAGGACACACAGCGGA 305
 |||||

QY 121 TATGATTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCTCAATCATGGC 180
 |||||
 Db 306 TACGATTTTGAATTTGGAAGATTTACGGAATACCTCG---ATGACACTCAATAACGGC 362
 |||||

QY 181 GGTACGTTGAGTCCCAATGGAACAAATGTTTAAACAATATTTTCGTTAAAGTTAAAAA 240
 |||||
 Db 363 GGGGCAATTTAGTGCAGCTGGAACAAATATTTGGAATGCTTATTTGGAAGGAAAGAG 422
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QY 241 TTCAATGAACAAACACACACCAACAAAGTTGGTAAACATGTCCATAAAGTACGGAGCAAC 300
 |||||
 Db 423 TTTGATTCCACTAAACTCATCACTTGGCAACATCTCCATCAACTACACGAGCC 482
 |||||

QY 301 TTCCAAACAAATGTTAATGCGTATTATGCGTCTATGTTGAGTGTGACCTCTTGTGC 360
 |||||
 Db 483 TTTAACCCTGGCGGAATTCCTATTATGTTGCTATGGCTGGACACAATCTCCATTAGCT 542
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QY 361 GAATATATATTTGTCAGAGTTGGGGCAACTGGCTCCACAGGAGCAACGCTTAAGGG 420
 |||||
 Db 543 GAATACTACATTTGTTGAGTTCATGGGGCACATATCGTCCCAACAGG---AACGTATAAGGA 599
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QY 421 ACCATCACTGTTGATGAGGAAATATGATATCTACAGACTCTTAGAGTCAATCAACCC 480
 DB 600 TCATTTATGCGGATGAGGACATATGACATATATGAAACGCTCCGTGTCATCAACCT 659
 QY 481 TCCATTAGGGGATTGCCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACG 540
 DB 660 TCTATCATTTGGAGACGCTACCTTCAACAATATTGGAGTGTACGTCAACAAACGACCA 719
 QY 541 AGTGGCAGATTTCTGTGACCAACACTTTTAGAGCGTGGGAAACTTTAGGATGAATG 600
 DB 720 AGCGGAACGGTCTCCGTGAGTACGATTTTAAAAAATGGGAAAGCTTAGGCGATGCCAATG 779
 QY 601 GGGAAATGATGAGTGGCGCTTACTGTGAGAGGCTTCAAACTAGCGGAGTGTCTAAT 660
 DB 780 GGAATAATGATGAACACAGCAATTAACCTGTGAGAGGCTTACCGAAGCAACGGAAGTGGCAAT 839
 QY 661 GTATATAGCAATACATAAGAAATTAACGGTAAACCTCTCTCAACTATTAGTAA 713
 DB 840 GTCATGACGAATCAGCTGATGATTTCGATAAAGCATATGAANAAGCCAGCA 892

RESULT 12

AAZ51821
 ID AAZ51821 standard; DNA; 2364 BP.

AC AAZ51821;

XX 04-JUL-2000 (first entry)

XX Clostridium stercorarium xylanase A DNA.

XX Xylanase A; XynA; cellulosome; feruloyl esterase; phenolic acid esterase;
 KW thermostable; ferulic acid; wheat bran; agricultural byproduct; treat;
 KW grass; paper and pulp industry; feed processing; food additive;
 KW plant cell wall material; degradation; ds.

XX Clostridium stercorarium.

XX Key Location/Qualifiers
 FT CDS 440..1978
 FT /*tag= e
 FT /product= "Xylanase A"

XX WO200014243-A1.

XX 16-MAR-2000.

XX 03-SEP-1999; 99WO-US020304.

XX 04-SEP-1998; 98US-0099136P.

XX (UYGB-) UNIV GEORGIA RES FOUND INC.

XX Blum DL, Kataeva I, Li X, Ljungdahl LG;

XX WPI; 2000-256991/22.

XX P-PSDB; AAY70523.

XX New recombinant DNA molecule comprising a sequence encoding feruloyl
 PT esterase protein, useful for treating grasses and other plant materials
 PT used in pulp and paper industries, feed processing and food additives.

XX Disclosure; Page 97-99; 105pp; English.

XX The present sequence is a DNA encoding xylanase A (XynA) from Clostridium
 CC stercorarium. XynA contains family VI cellulose binding domain (CBD)
 CC which is homologous to the CBD of xylanase Z (XynZ) of Clostridium
 CC thermocellum. XynZ is an enzymatic component of C. thermocellum
 CC cellulosome and has a multi-domain structure which includes a dockerin
 CC domain, a catalytic xylanase domain, a family VI cellulose binding domain
 CC and a domain of unknown function. The unknown domain in the N-terminal
 CC region of XynZ has been found to contain feruloyl (phenolic acid)
 CC esterase which is involved in the degradation of plant cell wall

CC material. The novel feruloyl esterase is thermostable, easy to purify,
 CC has high temperature optima and stable over a wide pH range. The enzyme
 CC is used for producing ferulic acid from wheat bran or agricultural
 CC byproducts, treating grasses or other plant materials used in the pulp
 CC and paper industries, in feed processing and as a food additive
 XX Sequence 2364 BP; 791 A; 428 C; 458 G; 687 T; 0 U; 0 Other;

Query Match 34.4%; Score 255.6; DB 3; Length 2364;

Best Local Similarity 65.1%; Pred. No. 3.8e-65; Indels 6; Gaps 2;

Matches 410; Conservative 0; Mismatches 214;

QY 69 AATAATTTCAGGCACAAATCGTCACCGACAAATTCATTGGCAACCAACGATGGCTATGATTA 128

DB 520 AGTACTCGCGGGCGAATAATTTACGCAATAGACAGGACACATATGGAGGCTACGACTA 579

QY 129 TGAATTTTGGAAAGATAGCGGTGCTCTGGGACAATGATTTCTCAATCANTGGCGGTACGTT 198

DB 580 TGAGCTCTGGAAAGA---CTACGGAATACGATTATGGAACCTTAACGACGGTGGTACTTT 636

QY 189 CAGTGGCCCATGGAAACAATGTTAAACAATATTTTCCTGTAAGGTAAATAATTTCAATGA 248

DB 637 TAGTTGTCAATGGAGTAATATCGTAAATGCACTATTTAGAAAAGGAGAAATTTAATTC 696

QY 249 AACACAAACACACAAAGTGTGTAACATGTCCTATAAACTACGGAGCCAACTTCCAACC 308

DB 697 CGACAAACCTATCAAGNAATTAGGAGACATAGTAGTTGAATATGGCTGTGATTACAATCC 756

QY 309 AATGTAATCGTATTTATGCTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTA 368

DB 757 AAACGGAAATTCCTATTTGTTGTTTACCGTTGGACAAGAAATCCACTGGTTGAATATTA 816

QY 369 TATTGTGACAGTTGGGGCAACTGGGCTCCACAGAGCAACGCCTAAGGGGACCATCAC 428

DB 817 CATTTAGAAAAGCTGGGGCAGCTGGGCTCCACTGGAGCAACACCCBAAGGAACCATCAC 876

QY 429 TG---TTGATGGAGGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCTCCAT 485

DB 877 ACAGTGGATGGCAGGTACTTTATGAATATATGAAACTTACCCGGGTAAATCAGCCTTCCAT 936

QY 486 TAAGGGGATTTGCCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGG 545

DB 937 CGATGGAACCTGGGACATTTCCAAACAATATGGAGTGTTCGTACATCCAAAGAACCAACGG 996

QY 546 CACGATTTCTGTGACGAACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATGGGAA 605

DB 997 AACATATCTGTCACTGAACATTTTAAACAGTGGGAAAGAAATGGGCATGCGAATGGGTAA 1056

QY 606 AATGATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAATGATTA 665

DB 1057 GATGATGAAGTTGCTCTTACCGTTGAAGGTTATCAGAGCAGTGGGTACGCTAATGATTA 1116

QY 666 TAGCAATACATGAATTAACGGTAAACCC 695

DB 1117 CAAGAATGAATCAGAATAGGTGCAATCC 1146

RESULT 13

AAZ90972

ID AAZ90972 standard; DNA; 1190 BP.

XX AAT90972;

XX 22-MAY-1998 (first entry)

XX Nucleotide sequence encoding an enzyme with xylanase activity.

XX xynB gene; xylanase; enzyme; Dictyoglomus thermophilum strain R-46B.1;

XX G-Xylanase; beta -1,4-xylanase activity; activity; thermal stability;

XX biological bleaching; cellulose product; paper pulp; ss.

XX Dictyoglomus thermophilum.

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 17:09:58 ; Search time 85.4689 Seconds
(without alignments)
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Title: US-09-909-207-4
Perfect score: 744
Sequence: 1 ATGACACAAAGAAATTGAC.....TAACTTTGGATATAAAACAAT 744

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/1/ina/backfileseq1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	744	100.0	744	3	US-08-470-953A-4
2	744	100.0	744	3	US-08-470-953A-5
3	744	100.0	1513	3	US-08-470-953A-10
4	744	100.0	1513	3	US-08-470-953A-11
5	713.6	95.9	744	3	US-09-189-060B-1
6	713.6	95.9	871	1	US-08-698-978-1
7	671.6	90.3	744	3	US-08-501-126-18
8	663	89.1	663	3	US-08-470-953A-1
9	663	89.1	663	3	US-08-470-953A-2
10	587.2	78.9	744	3	US-09-189-060B-11
11	273	36.7	1022	3	US-08-275-526C-1
12	273	36.7	1022	3	US-08-275-526C-35
13	273	36.7	1022	4	US-09-076-677-1
14	273	36.7	1022	4	US-09-076-677-35
15	273	36.7	1022	4	US-09-073-055-1
16	273	36.7	1022	4	US-09-073-055-35
17	272.8	36.7	681	3	US-08-275-526C-30
18	272.8	36.7	681	3	US-08-275-526C-32
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20	272.8	36.7	681	4	US-09-076-677-32
21	272.8	36.7	681	4	US-09-073-055-30
22	272.8	36.7	681	4	US-09-073-055-32
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24	255.6	34.4	2364	4	US-09-603-311-23
25	255	34.3	600	3	US-08-275-526C-26
26	255	34.3	600	3	US-08-275-526C-34
27	255	34.3	600	4	US-09-076-677-26

28	255	34.3	600	4	US-09-076-677-34
29	255	34.3	600	4	US-09-073-055-26
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32	154.4	20.8	164	3	US-08-501-126-15
33	154.4	20.8	164	3	US-08-501-126-16
34	132.4	17.8	294	3	US-08-817-946-4
35	132.4	17.8	294	4	US-09-639-354A-4
36	119.4	16.0	1375	2	US-08-468-812-1
37	119.4	16.0	1375	3	US-08-590-563-1
38	119.4	16.0	1375	4	US-09-770-621-1
39	119.4	16.0	1375	4	US-09-233-832-1
40	119	16.0	229	3	US-09-189-060B-53
41	118.4	15.9	573	1	US-08-709-912-18
42	118.4	15.9	573	2	US-09-047-370-18
43	117.8	15.8	1207	1	US-08-575-964-2
44	117.8	15.8	1207	1	US-08-963-500-2
45	115.2	15.5	213	3	US-09-189-060B-49

ALIGNMENTS

RESULT 1
US-08-470-953A-4
; Sequence 4, Application US/08470953A
; Patent No. 6346407

; GENERAL INFORMATION:

; APPLICANT: ANDREE LAHAYE

; APPLICANT: ERIC DE BUYL

; APPLICANT: PIERRE LEDOUX

; APPLICANT: RENE DETROZ

; TITLE OF INVENTION: xylanase, microorganisms produced it.

; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

; and uses thereof

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESS: WILLIAM BRINKS HOFER GILSON & LIONE

; STREET: 2000 K St., N.W., Suite 200

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,953A

; FILING DATE: 6-OCTOBER-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Wilhem F. Gadiano, Esq.

; REGISTRATION NUMBER: 37,136

; REFERENCE/DOCKET NUMBER: 4121-40

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-429-0625

; TELEFAX: (202) 293-1850

; TELEX: 650 383-5605

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 744 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; STRAIN: Bacillus

US-08-470-953A-4

Query Match 100.0%; Score 744; DB 3; Length 744;
Best Local Similarity 100.0%; Pred. No. 9e-223;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACACAAAGAAATTCAGCGTGTGATTTTACGCTTTTGTAGTTTGTGTTTGTGCACTAACCTTA 60
DB 1 ATGACACAAAGAAATTCAGCGTGTGATTTTACGCTTTTGTAGTTTGTGTTTGTGCACTAACCTTA 60

QY 61 CCTCAGAAATAATTCAGGCAAAATCGTCACCGAATTCATTCATGGCAACACGATGGC 120
DB 61 CCTCAGAAATAATTCAGGCAAAATCGTCACCGAATTCATTCATGGCAACACGATGGC 120

QY 121 TATGATTATGAATTTTGGAAAGATAGCGTGTGCTCGGACAAATGATTTCTCAATCATGGC 180
DB 121 TATGATTATGAATTTTGGAAAGATAGCGTGTGCTCGGACAAATGATTTCTCAATCATGGC 180

QY 181 GGTACGTTTCAGTCCCAATGGAAACAATGTTTAAACAACATATTTCCGTAAGGTTAAAAA 240
DB 181 GGTACGTTTCAGTCCCAATGGAAACAATGTTTAAACAACATATTTCCGTAAGGTTAAAAA 240

QY 241 TTCAATGAACACAAACACACACCAATGGTGGTGAACATGTCATTAACACTACGGAGCCAC 300
DB 241 TTCAATGAACACAAACACACACCAATGGTGGTGAACATGTCATTAACACTACGGAGCCAC 300

QY 301 TTCCAAACCAATGTAATGCGTGTGATTTATGCGTGTGATGTTGACCTCTTGTGTC 360
DB 301 TTCCAAACCAATGTAATGCGTGTGATTTATGCGTGTGATGTTGACCTCTTGTGTC 360

QY 361 GAAATATTATTTGTCAGACATGGGGCAACTGGCGTCCACGAGGACACGCTTAAGGG 420
DB 361 GAAATATTATTTGTCAGACATGGGGCAACTGGCGTCCACGAGGACACGCTTAAGGG 420

QY 421 ACCATCCTGTTGATGGAGAACATATGATATCTACGAGCTCTTAGAGTCAATCAACCC 480
DB 421 ACCATCCTGTTGATGGAGAACATATGATATCTACGAGCTCTTAGAGTCAATCAACCC 480

QY 481 TCCATTAGGGGATGGCCACATTTTAAACAATTTGGAGTGTTCGAAGATCGAAAGCGACG 540
DB 481 TCCATTAGGGGATGGCCACATTTTAAACAATTTGGAGTGTTCGAAGATCGAAAGCGACG 540

QY 541 AGTGCCAGATTTCTGTGACCAACCACTTTAGAGCGTGGGAAACTTAGGATGAATATG 600
DB 541 AGTGCCAGATTTCTGTGACCAACCACTTTAGAGCGTGGGAAACTTAGGATGAATATG 600

QY 601 GGGAAATCTAGATCGCGTTACTGTAGAGGCTATCAAGCTACGAGTGCCTAAT 660
DB 601 GGGAAATCTAGATCGCGTTACTGTAGAGGCTATCAAGCTACGAGTGCCTAAT 660

QY 661 GTATATAGCAATACACTAAGAAATTAACCGTAAACCTCTCTCAACTATTAGTAATGACGAG 720
DB 661 GTATATAGCAATACACTAAGAAATTAACCGTAAACCTCTCTCAACTATTAGTAATGACGAG 720

QY 721 AGCATAACTTTGGATAAAAAACAAT 744
DB 721 AGCATAACTTTGGATAAAAAACAAT 744

RESULT 2

US-08-470-953A-5
; Sequence 5, Application US/08470953A
; Patent No. 6346407
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; APPLICANT: ERIC DE BUYL
; APPLICANT: PIERRE LEDOUX
; APPLICANT: RENE DETROZ
; TITLE OF INVENTION: xylanase, microorganisms produced it,
; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
; TITLE OF INVENTION: and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE

STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
FEATURE:
NAME/KEY: mat peptide
LOCATION: 82..744
FEATURE:
NAME/KEY: sig peptide
LOCATION: 1..81
US-08-470-953A-5

Query Match 100.0%; Score 744; DB 3; Length 744;
Best Local Similarity 100.0%; Pred. No. 9e-223;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACACAAAGAAATTCAGCTTTCATTTTACGCTTTTGTAGTTTGTGTTTGTGCACTAACCTTA 60
DB 1 ATGACACAAAGAAATTCAGCTTTCATTTTACGCTTTTGTAGTTTGTGTTTGTGCACTAACCTTA 60

QY 61 CCTCAGAAATAATTCAGGCAAAATCGTCACCGAATTCATTCATGGCAACACGATGGC 120
DB 61 CCTCAGAAATAATTCAGGCAAAATCGTCACCGAATTCATTCATGGCAACACGATGGC 120

QY 121 TATGATTATGAATTTTGGAAAGATAGCGTGTGCTCGGACAAATGATTTCTCAATCATGGC 180
DB 121 TATGATTATGAATTTTGGAAAGATAGCGTGTGCTCGGACAAATGATTTCTCAATCATGGC 180

QY 181 GGTACGTTTCAGTCCCAATGGAAACAATGTTTAAACAACATATTTCCGTAAGGTTAAAAA 240
DB 181 GGTACGTTTCAGTCCCAATGGAAACAATGTTTAAACAACATATTTCCGTAAGGTTAAAAA 240

QY 241 TTCAATGAACACAAACACACACCAATGGTGGTGAACATGTCATTAACACTACGGAGCCAC 300
DB 241 TTCAATGAACACAAACACACACCAATGGTGGTGAACATGTCATTAACACTACGGAGCCAC 300

QY 301 TTCCAAACCAATGTAATGCGTGTGATTTATGCGTGTGATGTTGACCTCTTGTGTC 360
DB 301 TTCCAAACCAATGTAATGCGTGTGATTTATGCGTGTGATGTTGACCTCTTGTGTC 360

QY 361 GAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACGAGGCAACGCCTAAGGG 420
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 GAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACGAGGCAACGCCTAAGGG 420
QY 421 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACC 480
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACC 480
QY 481 TCCATTAAGGGATTGCCACATTTAAACAATATGGAGTGTTCGAAGATCGAAACGCCAG 540
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 TCCATTAAGGGATTGCCACATTTAAACAATATGGAGTGTTCGAAGATCGAAACGCCAG 540
QY 541 AGTGGCAGATTTCTGTGACGCAACACATTTAGAGGTGGGAAAATTAGGGATGAATATG 600
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 AGTGGCAGATTTCTGTGACGCAACACATTTAGAGGTGGGAAAATTAGGGATGAATATG 600
QY 601 GGGAAAATGATGAAGTGCAGTCTTACTGTGAGAGGCTATCAAGTAGCGGAAGTCTAAT 660
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 GGGAAAATGATGAAGTGCAGTCTTACTGTGAGAGGCTATCAAGTAGCGGAAGTCTAAT 660
QY 661 GTATATAGCAATACACTAAGATTTACGGTAACCCCTCTCACTATTAGTAATGACGAG 720
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 GTATATAGCAATACACTAAGATTTACGGTAACCCCTCTCTCACTATTAGTAATGACGAG 720
QY 721 AGCATAACTTTGGATAAAAAACAAT 744
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 AGCATAACTTTGGATAAAAAACAAT 744

RESULT 3

US-08-470-953A-10
; Sequence 10, Application US/08470953A
; Patent No. 6346407
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; APPLICANT: ERIC DE BUHL
; APPLICANT: PIERRE LEDOUX
; APPLICANT: RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
; TITLE OF INVENTION: and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 6-OCTOBER-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1513 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
US-08-470-953A-10
Query Match 100.0%; Score 744; DB 3; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGACAAAAGAAATTCAGCTGATTTTACGCTTTTGTAGCTTTTGTGCTACTAACCTTA 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
620 ATGAGACAAAAGAAATTCAGCTGATTTTACGCTTTTGTAGCTTTTGTGCTACTAACCTTA 679
QY 61 CCTGCGAAATAATTCAGGCAAAATCGTACCAGCAATTCATTTGGCAACCAACCATGCG 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
680 CCTGCGAAATAATTCAGGCAAAATCGTACCAGCAATTCATTTGGCAACCAACCATGCG 739
QY 121 TATGATTAATGAATTTTGGAAAAGATAGCGGTGGCTCTGGGACAAATGATTTCTCAATCATGCG 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
740 TATGATTAATGAATTTTGGAAAAGATAGCGGTGGCTCTGGGACAAATGATTTCTCAATCATGCG 799
QY 181 GGTACGTTTCAGTGCCCAATGGAAACAATGTTTAAACAATATTTATTCGCTAAAGGTAATAAA 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
800 GGTACGTTTCAGTGCCCAATGGAAACAATGTTTAAACAATATTTATTCGCTAAAGGTAATAAA 859
QY 241 TTCANTGAACACAAACACACCAACAGTTCGTACATGTCCTCAATAAATCTACGAGGCAAC 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
860 TTCANTGAACACAAACACACCAACAGTTCGTACATGTCCTCAATAAATCTACGAGGCAAC 919
QY 301 TTCCAAACCAAAATGGTAATGCGTATTTATGCGTCTATGTTGGACTGTTTGACCCCTCTTGTG 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
920 TTCCAAACCAAAATGGTAATGCGTATTTATGCGTCTATGTTGGACTGTTTGACCCCTCTTGTG 979
QY 361 GAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACGAGGCAACGCCTAAGGG 420
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
980 GAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACGAGGCAACGCCTAAGGG 1039
QY 421 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACC 480
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1040 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACC 1099
QY 481 TCCATTAAGGGATTGCCACATTTAAACAATATGGAGTGTTCGAAGATCGAAACGCCAG 540
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1100 TCCATTAAGGGATTGCCACATTTAAACAATATGGAGTGTTCGAAGATCGAAACGCCAG 1159
QY 541 AGTGGCAGATTTCTGTGACGCAACCACTTTAGAGGTGGGAAAATTAGGGATGAATATG 600
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1160 AGTGGCAGATTTCTGTGACGCAACCACTTTAGAGGTGGGAAAATTAGGGATGAATATG 1219
QY 601 GGGAAAATGATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAAT 660
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1220 GGGAAAATGATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAAT 1279
QY 661 GTATATAGCAATACACTAAGATTTACGGTAACCCCTCTCTCACTATTAGTAATGACGAG 720
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1280 GTATATAGCAATACACTAAGATTTACGGTAACCCCTCTCTCACTATTAGTAATGACGAG 1339
QY 721 AGCATAACTTTGGATAAAAAACAAT 744
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1340 AGCATAACTTTGGATAAAAAACAAT 1363

RESULT 4

US-08-470-953A-11
; Sequence 11, Application US/08470953A
; Patent No. 6346407
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; APPLICANT: ERIC DE BUHL
; APPLICANT: PIERRE LEDOUX
; APPLICANT: RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
NUMBER OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: 620...1363
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 701...1363
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 620...700

Db 860 TTCAATGAACACAAACACACACCAAGTTGGTAACATGTCCTCATAAACTACGGAGCAAC 919
Qy 301 TTCCAAACCAAAATGGTAATCGTATTTATCGGTCTATGGTGTGACTGTTGACCCCTCTGTGC 360
Db 920 TTCCAAACCAAAATGGTAATCGTATTTATCGGTCTATGGTGTGACTGTTGACCCCTCTGTGC 979
Qy 361 GAATATTATTTGTCGACAGTTGGGGCAACTGGCGTCCACAGGAGCAACGCCCTAAGGGG 420
Db 980 GAATATTATTTGTCGACAGTTGGGGCAACTGGCGTCCACAGGAGCAACGCCCTAAGGGG 1039
Qy 421 ACCATCACTGTTGATGGAGAACATATGATATCTACGAGACTTTAGAGTCAATCAACCC 480
Db 1040 ACCATCACTGTTGATGGAGAACATATGATATCTACGAGACTTTAGAGTCAATCAACCC 1099
Qy 481 TCATTAAAGGGGATTCGCACATTTAAACAATATTGAGTGTTCGAAGATCGAAACGCACG 540
Db 1100 TCATTAAAGGGGATTCGCACATTTAAACAATATTGAGTGTTCGAAGATCGAAACGCACG 1159
Qy 541 AGTGGCACGATTTCTGTGACGACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATG 600
Db 1160 AGTGGCACGATTTCTGTGACGACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATG 1219
Qy 601 GGGAAAATGTATGAAGTCGCGCTTACTGTAGAGAGGCTATCAAAAGTACGGAAGTCTAAT 660
Db 1220 GGGAAAATGTATGAAGTCGCGCTTACTGTAGAGAGGCTATCAAAAGTACGGAAGTCTAAT 1279
Qy 661 GTATATAGCAATACACATTAAGATTAACGGTAACCCCTCTCTCAACTATTAGTAAATGACGAG 720
Db 1280 GTATATAGCAATACACATTAAGATTAACGGTAACCCCTCTCTCAACTATTAGTAAATGACGAG 1339
Qy 721 AGCATAACTTTGGATAAAACAAT 744
Db 1340 AGCATAACTTTGGATAAAACAAT 1363

RESULT 5
US-09-189-060B-1
; Sequence 1, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Bacillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(744)
US-09-189-060B-1

Query Match 95.9%; Score 713.6; DB 3; Length 744;
Best Local Similarity 97.4%; Pred. No. 2.9e-213;
Matches 725; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 1 ATGAGACAAAAGAAATTCAGCGTTCGATTTTACGCTTTTGTAGTTTGTGTTTGTGACTAACCTTA 60
Db 1 ATGAGACAAAAGAAATTCAGCGTTCGATTTTACGCTTTTGTAGTTTGTGTTTGTGACTAACCTTA 60
Qy 61 CCTGCAGAAAATAATTCAGGCAAAATCGTACCGACAAATTCATCCAGCAAAATTCATGGCAACCGATGGC 120
Db 61 CCTGCAGAAAATAATTCAGGCAAAATCGTACCGACAAATTCATCCAGCAACCGATGGC 120

Qy 1 ATGAGACAAAAGAAATTCAGCGTTCGATTTTACGCTTTTGTAGTTTGTGTTTGTGACTAACCTTA 60
Db 620 ATGAGACAAAAGAAATTCAGCGTTCGATTTTACGCTTTTGTAGTTTGTGTTTGTGACTAACCTTA 679
Qy 61 CCTGCAGAAAATAATTCAGGCAAAATCGTACCGACAAATTCATCCAGCAACCGATGGC 120
Db 680 CCTGCAGAAAATAATTCAGGCAAAATCGTACCGACAAATTCATCCAGCAACCGATGGC 739
Qy 121 TATGATTATGAATTTTGGAAAGATAGCGGTGCTCTGGACAAATGATCTCAATCATGCG 180
Db 740 TATGATTATGAATTTTGGAAAGATAGCGGTGCTCTGGACAAATGATCTCAATCATGCG 799
Qy 181 GGTACGTTTCAGTCCCAATGGAAACATGTTAAACAATATTATTCGTAAGGTAAGAAAA 240
Db 800 GGTACGTTTCAGTCCCAATGGAAACATGTTAAACAATATTATTCGTAAGGTAAGAAAA 859
Qy 241 TTCAATGAACACAAACACACCAAGTTGGTAACATGTCCTCATAAACTACGGAGCAAC 300

Query Match 100.0%; Score 744; DB 3; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGACAAAAGAAATTCAGCGTTCGATTTTACGCTTTTGTAGTTTGTGTTTGTGACTAACCTTA 60
Db 620 ATGAGACAAAAGAAATTCAGCGTTCGATTTTACGCTTTTGTAGTTTGTGTTTGTGACTAACCTTA 679
Qy 61 CCTGCAGAAAATAATTCAGGCAAAATCGTACCGACAAATTCATCCAGCAACCGATGGC 120
Db 680 CCTGCAGAAAATAATTCAGGCAAAATCGTACCGACAAATTCATCCAGCAACCGATGGC 739
Qy 121 TATGATTATGAATTTTGGAAAGATAGCGGTGCTCTGGACAAATGATCTCAATCATGCG 180
Db 740 TATGATTATGAATTTTGGAAAGATAGCGGTGCTCTGGACAAATGATCTCAATCATGCG 799
Qy 181 GGTACGTTTCAGTCCCAATGGAAACATGTTAAACAATATTATTCGTAAGGTAAGAAAA 240
Db 800 GGTACGTTTCAGTCCCAATGGAAACATGTTAAACAATATTATTCGTAAGGTAAGAAAA 859
Qy 241 TTCAATGAACACAAACACACCAAGTTGGTAACATGTCCTCATAAACTACGGAGCAAC 300

541 AGTGGCAGATTCTGTGACCAACACCTTTAGAGCGTGGGAAACCTTAGGATGAATATG 600
 541 AGTGGCAGATTCTGTGACCAACACCTTTAGAGCGTGGGAAACCTTAGGATGAATATG 600
 601 GGGAAATGATGATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT 660
 601 GGGAAATGATGATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT 660
 661 GTATATAGCAATACACTAAGAAATTAACGGTAAACCCCTCTCAACTATTAGTAATGACAAG 720
 661 GTATATAGCAATACACTAAGAAATTAACGGTAAACCCCTCTCAACTATTAGTAATGACAAG 720
 721 AGCATAACTTTGGTATAAAACAAT 744
 721 AGCATAACTTTAGTATAAAACAAT 744

RESULT 7
 US-08-501-126-18
 ; Sequence 18, Application US/08501126
 ; Patent No. 6140095
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Solingen, Pieter
 ; APPLICANT: Williams, Diane P.
 ; APPLICANT: Iverson, Sara
 ; APPLICANT: Farrell, Roberta L.
 ; APPLICANT: Herbes, Wilhelmina T.
 ; APPLICANT: Van Der Kleij, Wilhelmus A.
 ; APPLICANT: Herweijer, Margaretha A.
 ; APPLICANT: Van Beckhoven W.C., Rudolf F.
 ; APPLICANT: Quax, Wilhelmus J.
 ; APPLICANT: Jones, Brian E.
 ; TITLE OF INVENTION: ALKALI-TOLERANT XYLANASES
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESS: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Avenue, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/501.126
 ; FILING DATE: 29-DEC-1995
 ; CLASSIFICATION: 425
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 4615-0057.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 887-1500
 ; TELEFAX: (202) 887-0763
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 744 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; STRAIN: 1-43-3
 ; INDIVIDUAL ISOLATE: CBS672.93
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..744
 ; OTHER INFORMATION: /product= "xylanase"

US-08-501-126-18
 Query Match 90.3%; Score 671.6; DB 3; Length 744;
 Best Local Similarity 95.7%; Pred. No. 4e-200;
 Matches 712; Conservative 0; Mismatches 29; Indels 3; Gaps 2;
 QY 1 ATGAGACAAAAGAAATGACGTTGATTTAGCCCTTTTATAGTTTGTGTTTGTGACCTTA 60
 DB 1 ATGAGCCAAAAGAAATGACGTTGA--TTAACCTTTTATAGTTTGTGTTTGTGACCTTA 57
 QY 61 CTGCGAGAAATATTCAGGCACAAAATCGTCACCGACAATTCATTCGTCGACCAACGATGC 120
 DB 58 CTGCGAAGATTAAGTCAGGCACAAAATCGTCACCGACAATTCATTCGTCGACCAACGATGC 117
 QY 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGC 180
 DB 118 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGC 177
 QY 181 GGTACGTTTCAGTGCCTCAATGGAAACAATGTTTAAACAATATTTATTCGGTAAAGGTAAAAA 240
 DB 178 GGTACGTTTCAGTGCCTCAATGGAAACAATGTTTAAACAATATTTATTCGGTAAAGGTAAAAA 237
 QY 241 TTCAATGAAAACACAAACACACACCAACCAAGTTGGTAAACATGTCCTAATAACTACGGACCAAC 300
 DB 238 TTCAATGAAAACACAAACACACACCAACCAAGTTGGTAAACATGTCCTAATAACTACGGACCAAC 297
 QY 301 TTCCAACCAATGTAATGCGTATTTATGCGTCTATGTTGGACTGTGTGACCCCTCTTTGTC 360
 DB 298 TTCCAGCCAAAACGGTAATGCGTATTTATGCGTCTATGTTGGACTGTGTGACCCCTCTTTGTC 357
 QY 361 GAATATTATATTGTGACAGTTGGGGCAACTGGGCGTCCACAGAGCAACGCTTAAGGGG 420
 DB 358 GAATATTATATTGTGACAGTTGGGGCAACTGGGCGTCCACAGAGCAACGCTTAAGGGG 417
 QY 421 ACCATCACTGTTGATGAGGAAACATATGATATCTATGAAACTCTTTAGAGTCAATCAGCCC 480
 DB 418 ACCATCACTGTTGATGAGGAAACATATGATATCTATGAAACTCTTTAGAGTCAATCAGCCC 477
 QY 481 TCCATTAAAGGGGATTGCCACATTTAAACAATATTGGAAGTGTTCGAAGATCGAAACGACG 540
 DB 478 TCCATTAAAGGGGATTGCCACATTTAAACAATATTGGAAGTGTTCGAAGATCGAAACGACG 537
 QY 541 AGTGGCAGATTCTGTGACCAACCACTTTAGAGCGTGGGAAACCTTAGGATGAATATG 600
 DB 538 AGTGGCAGATTCTGTGACCAACCACTTTAGAGCGTGGGAAACCTTAGGATGAATATG 597
 QY 601 GGGAAATGATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT 660
 DB 598 GGGAAATGATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT 657
 QY 661 GTATATAGCAATACACTAAGAAATTAACGGTAAACCCCTCTCAACTATTAGTAATGACAAG 720
 DB 658 GTATATAGCAATACACTAAGAAATTAACGGTAAACCCCTCTCAACTATTAGTAATGACAAG 717
 QY 721 AGCATAACTTTGGTATAAAACAAT 744
 DB 718 AGCATAACTTTAGTATAAAACAAT 741

RESULT 8
 US-08-470-953A-1
 ; Sequence 1, Application US/08470953A
 ; Patent No. 6346407
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDREE LAHAVE
 ; APPLICANT: ERIC DE BUYL
 ; APPLICANT: PIERRE LEDOUX
 ; APPLICANT: FERE DETROZ
 ; TITLE OF INVENTION: Xylanase, microorganisms produced it,
 ; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
 ; TITLE OF INVENTION: and uses thereof
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:

ADDRESSER: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem P. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
US-08-470-953A-1

Query Match 89.1%; Score 663; DB 3; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.9e-197;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CAATCGTCCAGCAATATCCATTTGGCAACACGATGGCTATGATTAATGATTTTGGAAA 141
DB 1 CAATCGTCCAGCAATATCCATTTGGCAACACGATGGCTATGATTAATGATTTTGGAAA 60
QY 142 GATAGCGGTGGCTCTGGGCAATGATTTCAATCATGCGGGTACGTTTCAGTCCCAATGG 201
DB 61 GATAGCGGTGGCTCTGGGCAATGATTTCAATCATGCGGGTACGTTTCAGTCCCAATGG 120
QY 202 AACATGTTTAAACACATATATTCCTGTAAGGTAAATTTCAATGAACACACACACAC 261
DB 121 AACATGTTTAAACACATATATTCCTGTAAGGTAAATTTCAATGAACACACACACAC 180
QY 262 CAACAAGTTGGTAAACATGTCATAAACTACGAGCAACTTCCAAACCAATGTAATGCG 321
DB 181 CAACAAGTTGGTAAACATGTCATAAACTACGAGCAACTTCCAAACCAATGTAATGCG 240
QY 322 TATTTATGCGTCTATGGTTGATGTTGACCCCTCTTGTGCAATATATATTTGCGACAGT 381
DB 241 TATTTATGCGTCTATGGTTGATGTTGACCCCTCTTGTGCAATATATATTTGCGACAGT 300
QY 382 TGGGGCACTGGGCTCCACGAGCAACGCTTAAGGGACCATCACTGTTGATGGAGGA 441
DB 301 TGGGGCACTGGGCTCCACGAGCAACGCTTAAGGGACCATCACTGTTGATGGAGGA 360
QY 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCCAATTAAGGGATGTCACA 501
DB 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCCAATTAAGGGATGTCACA 420
QY 502 TTTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCGACGATTTCTGTGACG 561
DB 421 TTTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCGACGATTTCTGTGACG 480

RESULT 9

US-08-470-953A-2
; Sequence 2, Application US/08470953A
; Patent No. 6346407

GENERAL INFORMATION:

APPLICANT: ANDREE LAHAYE

APPLICANT: ERIC DE BUYL

APPLICANT: PIERRE LEDOUX

APPLICANT: RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: and uses thereof

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSER: WILLIAM BRINKS HOFER GILSON & LIONE

STREET: 2000 K St., N.W., Suite 200

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,953A

FILING DATE: 6-OCTOBER-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wilhem P. Gadiano, Esq.

REGISTRATION NUMBER: 37,136

REFERENCE/DOCKET NUMBER: 4121-40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-429-0625

TELEFAX: (202) 293-1850

TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 663 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

STRAIN: Bacillus

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 1..663

FEATURE:

NAME/KEY: CDS

LOCATION: 1..663

US-08-470-953A-2

QY 562 AACACATTAGAGCGTGGGAAACTTAGGGATGAATATGGGAAATATGATGAATCGCG 621
DB 481 AACACATTAGAGCGTGGGAAACTTAGGGATGAATATGGGAAATATGATGAATCGCG 540
QY 622 CTTACTGTAGAAGGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 681
DB 541 CTTACTGTAGAAGGCTATCAAGTAGCGGAAGTGTCTAATGTATATAGCAATACACTAAGA 600
QY 682 ATTAACGGTAACCCCTCTCTCAACTATTAGTAATGACGAGAGCATAAATTTGGATAAAAAAC 741
DB 601 ATTAACGGTAACCCCTCTCTCAACTATTAGTAATGACGAGAGCATAAATTTGGATAAAAAAC 660
QY 742 AAT 744
DB 661 AAT 663

```

Query Match      89.1%; Score 663; DB 3; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.9e-197;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CAAATCGTCACCGACAAATTCATTTGGCAACACGATGGCTATGATTGAATTTTGGAAA 141
DB 1 CAAATCGTCACCGACAAATTCATTTGGCAACACGATGGCTATGATTGAATTTTGGAAA 60

QY 142 GATAGCGGTGCTCTGGGCAATGATTTCTCAATCATGCGGTGACGTTGAGTCCCAATGG 201
DB 61 GATAGCGGTGCTCTGGGCAATGATTTCTCAATCATGCGGTGACGTTGAGTCCCAATGG 120

QY 202 ACAAATGTTAAACAATATTTTCGTTAAAGTAAATTTCAATGAACACACACAC 261
DB 121 ACAAATGTTAAACAATATTTTCGTTAAAGTAAATTTCAATGAACACACACAC 180

QY 262 CAACAAGTTGGTAACATGTCCTCAATAAATACGAGGCAACTTCCAAACCAATGGTAATCGG 321
DB 181 CAACAAGTTGGTAACATGTCCTCAATAAATACGAGGCAACTTCCAAACCAATGGTAATCGG 240

QY 322 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTTGTCGAATATATTTGTCGACAGT 381
DB 241 TATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTTGTCGAATATATTTGTCGACAGT 300

QY 382 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGA 441
DB 301 TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGA 360

QY 442 ACATATGATATACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGGCCACA 501
DB 361 ACATATGATATACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGGCCACA 420

QY 502 TTTAAACATATTTGAGTGTTCGAAGTTCGAAGTTCGAAGTTCGAAGTTCGAAGTTCGAAG 561
DB 421 TTTAAACATATTTGAGTGTTCGAAGTTCGAAGTTCGAAGTTCGAAGTTCGAAGTTCGAAG 480

QY 562 AACCACTTTAGAGCGTGGGAAACTTTAGGGATGAATATGGGAAATGTTGAAGTCCGG 621
DB 481 AACCACTTTAGAGCGTGGGAAACTTTAGGGATGAATATGGGAAATGTTGAAGTCCGG 540

QY 622 CTTACTGTAGAGGCTATCAAGTATAGCGGAAGTGTCAATATATATAGCAATACACTAAGA 681
DB 541 CTTACTGTAGAGGCTATCAAGTATAGCGGAAGTGTCAATATATATAGCAATACACTAAGA 600

QY 682 ATTAACGGTAACCCCTCTCTCAACTATTAGTATGACGAGACATACCTTTGGATAAAG 741
DB 601 ATTAACGGTAACCCCTCTCTCAACTATTAGTATGACGAGACATACCTTTGGATAAAG 660

QY 742 AAT 744
DB 661 AAT 663

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RESULT 10
US-09-189-060B-11
; Sequence 11, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 744

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; TYPE: DNA
; ORGANISM: Hybrid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(744)
US-09-189-060B-11

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Query Match      78.9%; Score 587.2; DB 3; Length 744;
Best Local Similarity 86.8%; Pred. No. 1e-173;
Matches 646; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATGAGACAAAAGAAATTTGACGTTGATTTTACGCTTTTGTGTTTGTGCTAACCTTA 60
DB 1 ATGAGACAAAAGAAATTTGACGTTGATTTTACGCTTTTGTGTTTGTGCTAACCTTA 60

QY 61 CCTCAGAAATAATTTTACGAGCAAAATCGTCACCGACAATTCATTGGCAACACGATGGC 120
DB 61 CCTCAGAAATAATTTTACGAGCAAAATCGTCACCGACAATTCATTGGCAACACGATGGC 120

QY 121 TATGATTATGAAATTTTGGAAAGATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGGC 180
DB 121 TATGATTATGAAATTTTGGAAAGATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGGC 180

QY 181 GGTACGTTTCAGTGGCCCAATGGAAACAATGTTAAACAATATTTATTCCTGTAAGGTAAAGAA 240
DB 181 GGTACGTTTCAGTGGCCCAATGGAAACAATGTTAAACAATATTTATTCCTGTAAGGTAAAGAA 240

QY 241 TTCAATGAAACACAAAACACACCAAGTTGGTAAACATGTCCTAATAAATACGAGGCAAC 300
DB 241 TTCAATGAAACACAAAACACACCAAGTTGGTAAACATGTCCTAATAAATACGAGGCAAC 300

QY 301 TTCCAAACCAATGTAATGCTATTTATGCTGCTATGCTGTTGGACTGTTGACCTCTTGTG 360
DB 301 TTCCAAACCAATGTAATGCTATTTATGCTGCTATGCTGTTGGACTGTTGACCTCTTGTG 360

QY 361 GAATATTTATTTGTCGACAGTTGGGGCAACTGGCGCTCCACGAGGCAACGCTTAAGGGG 420
DB 361 GAATATTTATTTGTCGACAGTTGGGGCAACTGGCGCTCCACGAGGCAACGCTTAAGGGG 420

QY 421 ACCATCACTGTTGATGAGGAAACATATGATATCTACAGACTCTTAGAGTCAATCAACCC 480
DB 421 ACCATCACTGTTGATGAGGAAACATATGATATCTACAGACTCTTAGAGTCAATCAACCC 480

QY 481 TCCATTAAAGGGATTTGCCACATTTAAACAATTTTGAAGTGTTCGAAGATCGAAACGCAAG 540
DB 481 TCCATTAAAGGGATTTGCCACATTTAAACAATTTTGAAGTGTTCGAAGATCGAAACGCAAG 540

QY 541 AGTGGCACGATTTTGTGTCAGCAACCACTTTTAGAGCGGTGGGAAAACCTTAGGGATGAATG 600
DB 541 AGTGGCACGATTTTGTGTCAGCAACCACTTTTAGAGCGGTGGGAAAACCTTAGGGATGAATG 600

QY 601 GGGGAAATGTTGATGAGTGGCTTACTGTAGAAGGCTATCAAGTACGAGGAGTCTTAAT 660
DB 601 GGGGAAATGTTGATGAGTGGCTTACTGTAGAAGGCTATCAAGTACGAGGAGTCTTAAT 660

QY 661 GTATATAGCAATACACTTAAGAATTTAAGGTAACCCCTCTCTCAACTATTAGTAAAGCAG 720
DB 661 GTATATAGCAATACACTTAAGAATTTAAGGTAACCCCTCTCTCAACTATTAGTAAAGCAG 720

QY 721 AGCAATACTTTGGATAAAAAACAAT 744
DB 721 AGCAATACTTTGGATAAAAAACAAT 744

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RESULT 11
US-08-275-526C-1
; Sequence 1, Application US/08275526C
; Patent No. 6180382
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: LAHAYE, ANDR E
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE

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; APPLICANT: DETROZ, REN
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,526C
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORGANISM: Bacillus pumilus
; STRAIN: PRL B12
; US-08-275-526C-1

Query Match 36.7%; Score 273; DB 3; Length 1022;
Best Local Similarity 63.4%; Pred. No. 2.4e-75;
Matches 452; Conservative 0; Mismatches 255; Indels 6; Gaps 2;

QY 1 ATGAGACAAAGAAATGGAGTTGATTTAGTCTTTTGGCTTTTGGTCTTAACTTA 60
DB 186 ATGAATTTGAAAGATTGAGCGTGTGTTGTGATGTGATTTGGATTGCTGACACTG 245
QY 61 CTGTGCAAAATAATTCAGGCACAAATCGTCACCGACAATTCATTTGGCAACACGATGCC 120
DB 246 ACGCTGTGCGCGTCATCGCGAAACGATTATGATAATAGGATAGGACACACGCGGA 305
QY 121 TATGATTGAAATTTGGAAAGATAGCGGTGGCTCTGGGACATGATTCATCATGCG 180
DB 306 TACGATTTTGAATATGGAAGATTACGGAATACCTCG--ATGACACTCAATAACGGC 362
QY 181 GGTACGTTGACGTCACCAATGTAACACATATTTTCCGTAAGTAAAGAA 240
DB 363 GGGGCAATTTAGTGAAGCTGGAACAATTTGGAATGCTTATTTGAAAGGAAGAG 422
QY 241 TTCAATGAACAAACACACACCAAGTTGGTAACATGTCCATAAATACGAGCAAC 300
DB 423 TTTGATTTCCATAAATCATCATCACTTGGCAACATCTCCATCAACTACACGCGC 482
QY 301 TTCACAAATAATGTTAATGCTATTTATGCTCTATGTTGGATGCTGTTACCTCTTGC 360
DB 483 TTTAACCCGGGGGAATTCCTATTTATGCTCTATGCTGGACACAAATCTCCATAGCT 542
QY 361 GAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACGAGCAACGCGCTAAGGG 420

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DB 543 GAATACTACATTTGTTGAGTCATGGGACACATATCGTCCAAACAGG--AACGTATAAAGGA 599
QY 421 ACCATCACTGTTGATGGAGGACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480
DB 600 TCATTTTATGCGGATGGAGGACATATGACATATATGAACGCTCCGTGTCAATCAGCCT 659
QY 481 TCCATTAAGGGGATGGCCACATTTTAAACAATATTCGAGTGTTCGAAGATCGAAACGACG 540
DB 660 TCTATCATTTGGAGAGCTACCTTCAACAATATTTGAGTGTACGTCAACAAACGACCA 719
QY 541 AGTGCCACGATTTCTGTGAGCAACACCTTTAGAGCGTGGGAAAACCTTAGGGATGAATATG 600
DB 720 AGCGGAACGGTCTCGTCACTGAGCATTTTAAAAAATGGAAAGCTTAGGCATGCCAATG 779
QY 601 GGGAAATGTATGAAGTCGCGTCTACTCTAGAGGCTATCAAGTAGCGGAGTGTCTAAT 660
DB 780 GGAATAATGTATGAACACAGCATTAATCTGTAGAGGCTACCGAAGCAACGGAAGTGGAA 839
QY 661 GTATATAGCAATACACTAAGAAATTAACGTAACCTCTCTCAACTATTAGTAA 713
DB 840 GTCATGACGATCAGCTGATGATTCGATAAAGCATATGAAAAAAGCCAGCA 892

RESULT 12
US-08-275-526C-35
; Sequence 35, Application US/08275526C
; Patent No. 6180382
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: LAHAYE, ANDR E
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE
; APPLICANT: DETROZ, REN
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,526C
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-08-275-526C-35

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Query Match 36.7%; Score 273; DB 3; Length 1022;
 Best Local Similarity 63.4%; Pred. No. 2.4e-75;
 Matches 452; Conservative 0; Mismatches 255; Indels 6; Gaps 2;

QY 1 ATGAGACAAAAGAAATTCAGCTTGATTTAGTCCCTTTTGTGTTTGTGCACTAACCTTA 60
 DB 186 ATGAATTTGAAGAGATTGAGCTGTTGTTGTGATGTTATGATTTGTGCTGACACTG 245

QY 61 CCTCAGAAATTAATTCAGGCAAAATGCTACCGCAATTCATTCGCAACACGATGGC 120
 DB 246 ACGGCTGTGCGGCTCATGCGAAACGATTTATGATAATAGGATAGGACACAGCGGA 305

QY 121 TATGATTAATGATTTTGAAGATAGCGTGGCTCTGGACAAATGATTTCAATCATGGC 180
 DB 306 TACGATTTGAATTTATGGAAGATTACGGAATACCTCG---ATGACACTCAATAACGGC 362

QY 181 GGTACGTTTCAGTCCCAATGGAACAATGTTTAAACAATATTTTCGTAAGGTAAGAAA 240
 DB 363 GGGCAATTTAGTCAAGCTGGAACAATATTGGAATGCTTTATTCGAAAAGGAAGAA 422

QY 241 TTCAATGAACAACAACAACACACCAATGTTGGTAACATGTCCTAATAACTACGAGCCAC 300
 DB 423 TTTGATTTCCACTAAAACCTCATCACTTGGCAACATCTCCATCAACTCAACGAGCC 482

QY 301 TTCCAAACCAATGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTT 360
 DB 483 TTTAAACCGGCGGGAATTCCTATTTATGTTATGTTATGTTATGTTATGTTATGTT 542

QY 361 GAATATTATATTTGTGACAGTTGGGCAACTGGCGTCCACAGGAGCAACCCCTAAGGG 420
 DB 543 GAATATTATATTTGTGACAGTTGGGCAACTGGCGTCCACAGG---AACGTATAAGGA 599

QY 421 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTAGAGCTCAATCAACC 480
 DB 600 TCATTTTATGCCGATGGAGGACATATGACATATATGAACGCTCCGCTCAATCAGCCT 659

QY 481 TCCATTAAGGGATTGGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAGCAG 540
 DB 660 TCTATCATTTGAGAGCGTACCTTTCAACAATATTGGAGTGTTCGAAGATCGAAGCAG 719

QY 541 AGTGCAGCATTTCTGTGAGCAACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATG 600
 DB 720 AGCGAAACGGTCTCGTCACTGAGCATTTTAAATAATGGAAGCTTAGGCGATGCAATG 779

QY 601 GGAATAATGATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAGTCTAAT 660
 DB 780 GGAATAATGATGAAGTCCGCTTACTGTAGAGGCTACCGAAGCAACGGAAGTCCGAAT 839

QY 661 GTATATAGCAATACACTAAGATTAACGTTAACGTTACCTCTCTCACTATTAGTAA 713
 DB 840 GTATATAGCAATACACTAAGATTTGATTTGATTAAGATATGAAAAGCCAGCA 892

RESULT 13
 US-09-076-677-1
 ; Sequence 1, Application US/09076677
 ; Patent No. 6423523
 ; GENERAL INFORMATION:
 ; APPLICANT: DE BUYL, ERIC
 ; LAHAYE, ANDREE
 ; LEDOUX, PIERRE
 ; AMORY, ANTOINE
 ; DETROZ, RENE
 ; ANDRE, CHRISTOPHE
 ; VETTER, ROMAN
 ;
 ; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
 ; EXPRESSION VECTORS FOR SUCH XYLANASE AND
 ; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 ; USE THEREOF
 ;
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOPFER GILSON & LIONE, P.C.

STREET: 2000 K St., N.W., Suite 200
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/076,677
 FILING DATE: 12-May-1998

CLASSIFICATION: <Unknown>
 APPLICATION NUMBER: US 08/275,526
 FILING DATE: 15-JUL-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Gadiano, Wilhem F.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-49

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 429-0625
 TELEFAX: (202) 293-0625
 TELEX: 650 383 5605

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1022 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Bacillus pumilus
 STRAIN: PRL B12
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-076-677-1

Query Match 36.7%; Score 273; DB 4; Length 1022;
 Best Local Similarity 63.4%; Pred. No. 2.4e-75;
 Matches 452; Conservative 0; Mismatches 255; Indels 6; Gaps 2;

QY 1 ATGAGACAAAAGAAATTCAGCTTGATTTAGTCCCTTTTGTGTTTGTGCACTAACCTTA 60
 DB 186 ATGAATTTGAAGAGATTGAGCTGTTGTTGTGATGTTATGATTTGTGCTGACACTG 245

QY 61 CCTCAGAAATTAATTCAGGCAAAATGCTACCGCAATTCATTCGCAACACGATGGC 120
 DB 246 ACGGCTGTGCGGCTCATGCGAAACGATTTATGATAATAGGATAGGACACAGCGGA 305

QY 121 TATGATTAATGATTTTGAAGATAGCGTGGCTCTGGACAAATGATTTCAATCATGGC 180
 DB 306 TACGATTTGAATTTATGGAAGATTACGGAATACCTCG---ATGACACTCAATAACGGC 362

QY 181 GGTACGTTTCAGTCCCAATGGAACAATGTTTAAACAATATTTTCGTAAGGTAAGAAA 240
 DB 363 GGGCAATTTAGTCAAGCTGGAACAATATTGGAATGCTTTATTCGAAAAGGAAGAA 422

QY 241 TTCAATGAACAACAACAACACCAATGTTGGTAACATGTCCTAATAACTACGAGCCAC 300
 DB 423 TTTGATTTCCACTAAAACCTCATCACTTGGCAACATCTCCATCAACTCAACGAGCC 482

QY 301 TTCCAAACCAATGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTT 360
 DB 483 TTTAAACCGGCGGGAATTCCTATTTATGTTATGTTATGTTATGTTATGTTATGTT 542

QY 361 GAATATTATATTTGTGACAGTTGGGCAACTGGCGTCCACAGGAGCAACCCCTAAGGG 420
 DB 543 GAATATTATATTTGTGACAGTTGGGCAACTGGCGTCCACAGG---AACGTATAAGGA 599

QY 421 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTAGAGCTCAATCAACC 480
 DB 600 TCATTTTATGCCGATGGAGGACATATGACATATATGAACGCTCCGCTCAATCAGCCT 659

Best Local Similarity 63.4%; Pred. No. 2.4e-75;
Matches 452; Conservative 0; Mismatches 255; Indels 6; Gaps 2;

QY 1 ATGAGACAAAGAAATTTGACGCTTTCATTTTACGCTTTTGTAGTTTGTGTTTGTGCACTAACCTTA 60
DB 186 ATGAAATTTGAAAGATTTGAGCTGTTGTTGTGATGTGATTTGATTTGTGCTGACACTG 245
QY 61 CCTCAGAAAATAATTCAGGCAAAATCGTCAACGCAATTCATTTGGCAACACGATGCG 120
DB 246 ACGCTGTGCGGCTCATGCGGAAACGATTTATGATAATAGGATAGGACACACAGCGGA 305
QY 121 TATGATTATGAAATTTGGAAAGATAGCGTGGCTCTGGGACAATGATTTCTCAATCATGCG 180
DB 306 TACGATTTTGAATTTATGGAAGGATTTACGGAATACTCTG---ATGACACTCAATAACGCG 362
QY 181 GGTACGTTTCACTGCGCAATGGAACAATGTTTAAACAATATTTATTCCTGTAAGGTTAAAAA 240
DB 363 GGGCAATTTAGTGCAAGCTGGAACAATATTTGGAATGCGCTTATTTTGGAAAGGAAGAAG 422
QY 241 TTCAATGAAACACAAACACACCAAGTTGGTAAACATGTCCATAAACTACGGAGCCAAAC 300
DB 423 TTTGATTTCCACTAAACTCATCATCACTTGGCAACATCTCCATCACTCAACACGACGC 482
QY 301 TTCCAAACCAAAATGTAATGCGTATTTATGCGTCTATGTTGGACTGTTGACCTCTTGTG 360
DB 483 TTTAAACCGCGGCGGAATTCCTATTTATGTTGCTCTATGCTGGACACAATCTCCATTAGCT 542
QY 361 GAATATTTATTTGCGACAGTTGGGCAACTGGGTCACACGAGGACCAACGCTTAAGGG 420
DB 543 GAATACTACATTTGTTAGTCATGCGGACATATGCTCCACAGG---AACGTATAAGGA 599
QY 421 ACCATCACTGTTGATGAGGAAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCC 480
DB 600 TCAATTTATGCGATGAGGACACATATGACATATATGAAACGCTCCGTTCAATCAGCCT 659
QY 481 TCCATTAAGGGATTTGCCACATTTTAAACAATTTGGAGTGTTCGAAGATCGAAACGACG 540
DB 660 TCTATCTGAGAGCGCTACCTTCAACAATATTTGAGTGTACGTCAAAACAAACGCA 719
QY 541 AGTGGCAGATTTCTGTCAGCAACACATTTAGAGCGTGGGAACTTAGGGATGAATATG 600
DB 720 ACGGAAACGGTCTCCGTCAGTGAGCATTTTAAATAATGGGAAGCTTAGGCATGCCAATG 779
QY 601 GGGAAATGTATGAAGTCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTCTAAT 660
DB 780 GGAATAATGTATGAAACAGCATTAATCTGTAGAGGCTACCGAAGCAACGGAAGTGCRAAT 839
QY 661 GTATATAGCAATACATAAGATTAACGTAACCTCTCTCACTATTAGTAA 713
DB 840 GTCATGACGAATCAGCTGATGATTCGATAAAGCATATGAAAAAAGCCAGCAA 892

QY 481 TCATTAAAGGGATTCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACG 540
DB 660 TCTATCTGAGAGCGCTACCTTTCAACAATATTGGAGTGTACGTCAACAACGCA 719
QY 541 AGTGCAGCATTTCTGTGTCAGCAACACATTTTAGAGCGTGGGAAACTTAGGGATGAATG 600
DB 720 ACGGAAACGGTCTCCGTCAGTGAGCATTTTAAATAATGGGAAGCTTAGGCATGCCAATG 779
QY 601 GGGAAATGTATGAAGTCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTGTCTAAT 660
DB 780 GGAATAATGTATGAAACAGCATTAATCTGTAGAGGCTACCGAAGCAACGGAAGTGCRAAT 839
QY 661 GTATATGCAATACATAAGATTAACGTAACCTCTCTCACTATTAGTAA 713
DB 840 GTCATGACGAATCAGCTGATGATTCGATAAAGCATATGAAAAAAGCCAGCAA 892

RESULT 14
US-09-076-677-35
; Sequence 35, Application US/09076677
; Patent No. 6423523
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; LAHAYE, ANDRE
; LEDOUX, PIERRE
; AMORY, ANTOINE
; DETROZ, RENE
; ANDRE, CHRISTOPHE
; VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; EXPRESSION VECTORS FOR SUCH XYLANASE AND
; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSER: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,677
; FILING DATE: 12-May-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,526
; FILING DATE: 15-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Willem P.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-076-677-35

Query Match 36.7%; Score 273; DB 4; Length 1022;

RESULT 15
US-09-073-055-1
; Sequence 1, Application US/09073055
; Patent No. 6426211
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; LAHAYE, ANDRE
; LEDOUX, PIERRE
; AMORY, ANTOINE
; DETROZ, RENE
; ANDRE, CHRISTOPHE
; VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; EXPRESSION VECTORS FOR SUCH XYLANASE AND
; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSER: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus pumilus
STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Job time : 86.4689 secs

Query Match 36.7%; Score 273; DB 4; Length 1022;
Best Local Similarity 63.4%; Pred. No. 2,4e-75;
Matches 452; Conservative 0; Mismatches 255; Indels 6; Gaps 2;

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QY 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAAATGATTCATCAATCATGGC 180
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QY 181 GGTACGTTTCAGTGCCCAATGGAACAATGTTTAAACATATATTTCGGTAAAGGTAAAAA 240
DB 363 GGGGCATTTAGTGCAAGCTGGAACAATATGGAAATGCTTATTTCGAAAAGGAAAGAG 422

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DB 423 TTTGATTCACATAAAACATCATCACTTGGCAACATCTCCATCAACTCAACGCGACC 482

QY 301 TTCACCAAAATGGTAATGCGTATTATTATGCGTCTATGGTTGGACTGTTGACCTCTTTGTC 360
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QY 361 GAATATTATATTGCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCCTTAAGGG 420
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QY 421 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480
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QY 481 TCCATTAAAGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAAGATCGAAACGCACG 540

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Db 720 AGCGGAACGGTCTCCGTCTAGTGAGCAATTTTAAAAAATGGGAAAGCTTTAGGCATGCCAATG 779
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Db 780 GGAATAATGTATGAACACAGCAATTAACCTGTAGAAGGCTACCGAAAGCAACGGAAGTGCGAAT 839
QY 661 GTATATAGCAATACACATAAGAAATTAACGGTAACCCCTCTCTCAACTATTAGTAA 713
Db 840 GTCATGAGCAATCAGCTGATGATTCGATAAAGCATATGAATAAAGCCAGCA 892

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 21:26:43 ; Search time 475.684 Seconds
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 7222084

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	744	100.0	744	US-09-909-207-5	Sequence 5, Appli
3	744	100.0	1513	US-09-909-207-10	Sequence 10, Appl
4	744	100.0	1513	US-09-909-207-11	Sequence 11, Appl
5	663	89.1	663	US-09-909-207-1	Sequence 1, Appli
6	663	89.1	663	US-09-909-207-2	Sequence 2, Appli
7	119.4	16.0	1375	US-09-770-621-1	Sequence 1, Appli
8	119.4	16.0	1375	US-10-286-993-1	Sequence 1, Appli
9	115.2	15.5	596	US-10-307-441-39	Sequence 39, Appl
10	111.4	15.0	942	US-10-213-990-71	Sequence 71, Appl
11	110	14.8	1002	US-10-213-990-70	Sequence 70, Appl
12	108.8	14.6	705	US-10-213-990-68	Sequence 68, Appl

13	106	14.2	2898	15	US-10-299-393-1	Sequence 1, Appli
14	104.8	14.1	712	14	US-10-213-990-64	Sequence 64, Appl
15	103.6	13.9	666	14	US-10-213-990-65	Sequence 65, Appl
16	96.8	13.0	739	14	US-10-213-990-67	Sequence 67, Appl
17	86.8	11.7	678	10	US-09-803-454-3	Sequence 3, Appli
18	84.2	11.3	1023	16	US-10-244-596-6	Sequence 6, Appli
19	84	11.3	1027	16	US-10-244-596-2	Sequence 2, Appli
20	83.2	11.2	645	15	US-10-237-386-10	Sequence 10, Appl
21	83.2	11.2	657	15	US-10-237-386-11	Sequence 11, Appl
22	82.6	11.1	1011	16	US-10-244-596-11	Sequence 13, Appl
23	82.6	11.1	1011	16	US-10-244-596-12	Sequence 12, Appl
24	82.6	11.1	1011	16	US-10-244-596-13	Sequence 13, Appl
25	82.6	11.1	1023	16	US-10-244-596-5	Sequence 5, Appli
26	82.6	11.1	1023	16	US-10-244-596-7	Sequence 7, Appli
27	82.6	11.1	1023	16	US-10-244-596-8	Sequence 8, Appli
28	82.6	11.1	1023	16	US-10-244-596-9	Sequence 9, Appli
29	81	10.9	81	9	US-09-909-207-7	Sequence 7, Appli
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35	77.8	10.5	1014	16	US-10-244-596-1	Sequence 1, Appli
36	77.2	10.4	749	18	US-10-425-115-82922	Sequence 82922, A
37	75.8	10.2	818	18	US-10-425-115-37173	Sequence 37173, A
38	73.8	9.9	850	18	US-10-425-115-177283	Sequence 177283, A
39	72.4	9.7	588	15	US-10-237-386-9	Sequence 9, Appli
40	72.4	9.7	983	9	US-09-467-368-1	Sequence 1, Appli
41	54.2	7.3	2054	15	US-10-419-969-5	Sequence 5, Appli
42	50.4	6.8	643	15	US-10-340-860A-39	Sequence 39, Appl
43	41	5.5	74	15	US-10-307-441-24	Sequence 24, Appl
44	40	5.4	557	9	US-09-970-616-1	Sequence 1, Appli
45	40	5.4	642	11	US-09-149-310-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-909-207-4
; Sequence 4, Application US/09090207
; Patent No. US20020115181A1

GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/909,207

APPLICATION NUMBER: 19-Jul-2001

FILING DATE: 19-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/470,953

FILING DATE: 06-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Wilhem F. Gadiano, Esq.

REGISTRATION NUMBER: 37,136

RESULT 2

US-09-909-207-5
; Sequence 5, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOPER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 82..744
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..81
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-909-207-5

Query Match 100.0%; Score 744; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 2.le-208;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-909-207-4

Query Match 100.0%; Score 744; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 2.le-208;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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481 QY TCCATTAAAGGGGATTCGCCAATTTAAACAATATTTGGAGTGTTCGAAAGATCGAAACGC 540
481 Db TCCATTAAAGGGGATTCGCCAATTTAAACAATATTTGGAGTGTTCGAAAGATCGAAACGC 540
541 QY AGTGCCACGATTCTCTGACGACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATG 600
541 Db AGTGCCACGATTCTCTGACGACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATG 600
601 QY GGGAAATATGATGAAGTCGCGTACTGTAGAGGCTATCAAGTAGTGGGAAATGCTAAT 660
601 Db GGGAAATATGATGAAGTCGCGTACTGTAGAGGCTATCAAGTAGTGGGAAATGCTAAT 660
661 QY GTATATGACAACTACATGAATTAACGTTACGCTTCTCACTATTATGATGACGAG 720
661 Db GTATATGACAACTACATGAATTAACGTTACGCTTCTCACTATTATGATGACGAG 720
721 QY AGCAATACCTTTGGATTAAGAAACAT 744
721 Db AGCAATACCTTTGGATTAAGAAACAT 744

RESULT 3

US-09-909-207-10
; Sequence 10, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOPPER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,207

; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1513 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-909-207-10

Query Match 100.0%; Score 744; DB 9; Length 1513;
Best Local Similarity 100.0%; Pred. No. 3e-208;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGACAAAGAAATGACGTTGATTTTGTAGCTTTTGTAGTTTGTGCTTAACCTTA 60
Db 620 ATGAGACAAAGAAATGACGTTGATTTTGTAGCTTTTGTAGTTTGTGCTTAACCTTA 679
QY 61 CTGCGAAGAAATTCAGGCACAAATCGTCACGCAATTCCTTGGACCAACCAATGATG 120
Db 680 CTGCGAAGAAATTCAGGCACAAATCGTCACGCAATTCCTTGGACCAACCAATGATG 739
QY 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACCAATGATTTCTCAATCATG 180
Db 740 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACCAATGATTTCTCAATCATG 799
QY 181 GGTACGTTTCAGTGGCCCAATGGAACAAATGTTAAACAATATTTCCGTAAGGTAAGAAA 240
Db 800 GGTACGTTTCAGTGGCCCAATGGAACAAATGTTAAACAATATTTCCGTAAGGTAAGAAA 859
QY 241 TTCATGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 300
Db 860 TTCATGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 919
QY 301 TTCCCAACCAATGTTAATGCGTATTTATGCGTCTATGTTGGACTGTTGACCCCTTTGTC 360
Db 920 TTCCCAACCAATGTTAATGCGTATTTATGCGTCTATGTTGGACTGTTGACCCCTTTGTC 979
QY 361 GAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACAGGAGCAACGGCTAAGGGG 420
Db 980 GAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACAGGAGCAACGGCTAAGGGG 1039
QY 421 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACC 480
Db 1040 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACC 1099
QY 481 TCCATTAAAGGGGATTCGCCAATTTAAACAATATTTGGAGTGTTCGAAAGATCGAAACGC 540
Db 1100 TCCATTAAAGGGGATTCGCCAATTTAAACAATATTTGGAGTGTTCGAAAGATCGAAACGC 1159
QY 541 AGTGCCACGATTCTCTGACGAAACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATG 600
Db 1160 AGTGCCACGATTCTCTGACGAAACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATG 1219
QY 601 GGGAAATATGATGAAGTCGCGTACTGTAGAGGCTATCAAGTAGTGGGAAATGCTAAT 660
Db 1220 GGGAAATATGATGAAGTCGCGTACTGTAGAGGCTATCAAGTAGTGGGAAATGCTAAT 1279

QY 661 GTATATAGCAATACACTAGAAATTAACGGTAAACCTCTCTCAACTATTAGTAATGACGAG 720
 DB 1280 GTATATAGCAATACACTAGAAATTAACGGTAAACCTCTCTCAACTATTAGTAATGACGAG 1339
 QY 721 AGCATAACTTTGGATAAAACAAT 744
 DB 1340 AGCATAACTTTGGATAAAACAAT 1363

RESULT 4

US-09-909-207-11
 ; Sequence 11, Application US/09909207
 ; Patent No. US20020115181A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDREE LAHAYE
 ; ERIC DE BUYL
 ; PIERRE LEDOUX
 ; RENE DETROZ
 ; TITLE OF INVENTION: Xylanase, microorganisms produced it,
 ; DNA molecule, processes for preparation of this xylanase
 ; and uses thereof
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
 ; STREET: 2000 K St., N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/909,207
 FILING DATE: 19-Jul-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/470,953
 FILING DATE: 06-JUNE-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilhem F. Gadiano, Esq.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-40
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-429-0625
 TELEFAX: (202) 293-1850
 TELEX: 650 383-5605

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1513 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 STRAIN: Bacillus

FEATURE:
 NAME/KEY: CDS
 LOCATION: 620..1363
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 701..1363
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 620..700

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-909-207-11
 Query Match 100.0%; Score 744; DB 9; Length 1513;
 Best Local Similarity 100.0%; Pred. No. 3e-208;
 Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACAAAAGAAATTGACGTTGATTTTATAGCCCTTTTATAGTTTGTGTTTGCACCTAACCTTA 60
 DB 620 ATGAGACAAAAGAAATTGACGTTGATTTTATAGCCCTTTTATAGTTTGTGTTTGCACCTAACCTTA 679
 QY 61 CCTGCAGAAAATAATTTCAGGCACAAAATCGTCACCGACAAATTCCTATTTGGCAACACGATGGC 120
 DB 680 CCTGCAGAAAATAATTTCAGGCACAAAATCGTCACCGACAAATTCCTATTTGGCAACACGATGGC 739
 QY 121 TATGATTATGAATTTTGGAAAAGATAGCGGTGGCTCTGGGACAATGATCTCAATCATGGC 180
 DB 740 TATGATTATGAATTTTGGAAAAGATAGCGGTGGCTCTGGGACAATGATCTCAATCATGGC 799
 QY 181 GGTACGTTTCAGTCCCAATGGAACAATGTTTAAACAATATTTTCCGTTAAAGGTAAAGAAA 240
 DB 800 GGTACGTTTCAGTCCCAATGGAACAATGTTTAAACAATATTTTCCGTTAAAGGTAAAGAAA 859
 QY 241 TTCAATGAAAACAAAACACACCAACCAAGTTGGTAAACATGTCCTATAAACTACGGAGCCAAC 300
 DB 860 TTCAATGAAAACAAAACACACCAACCAAGTTGGTAAACATGTCCTATAAACTACGGAGCCAAC 919
 QY 301 TTCCAAACCAATGGTAATGGTATTTATGGCTCTATGGTTGGACTGTGACCCCTCTTGTG 360
 DB 920 TTCCAAACCAATGGTAATGGTATTTATGGCTCTATGGTTGGACTGTGACCCCTCTTGTG 979
 QY 361 GATATTATATTTGTCGACAGTTGGGCAACTGGCGTCCACGAGGACAAACGCTTAAGGGG 420
 DB 980 GATATTATATTTGTCGACAGTTGGGCAACTGGCGTCCACGAGGACAAACGCTTAAGGGG 1039
 QY 421 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480
 DB 1040 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 1099
 QY 481 TCCATTAAGGGATGGCAATTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACG 540
 DB 1100 TCCATTAAGGGATGGCAATTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACG 1159
 QY 541 AGTGGCAGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATG 600
 DB 1160 AGTGGCAGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACCTTAGGATGAATATG 1219
 QY 601 GGGAAAATGTATGAAGTCGGCTTACTGTAGAAAGCTATCAAGTAGCGGAAGTGTAAAT 660
 DB 1220 GGGAAAATGTATGAAGTCGGCTTACTGTAGAAAGCTATCAAGTAGCGGAAGTGTAAAT 1279
 QY 661 GTATATAGCAATACACTAGAAATTAACGGTAAACCTCTCTCAACTATTAGTAATGACGAG 720
 DB 1280 GTATATAGCAATACACTAGAAATTAACGGTAAACCTCTCTCAACTATTAGTAATGACGAG 1339

RESULT 5

US-09-909-207-1
 ; Sequence 1, Application US/09909207
 ; Patent No. US20020115181A1
 ; GENERAL INFORMATION:

APPLICANT: ANDREE LAHAYE
 ERIC DE BUYL
 PIERRE LEDOUX
 RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,
 DNA molecule, processes for preparation of this xylanase
 and uses thereof

NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
 STREET: 2000 K St., N.W., Suite 200
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.

RESULT 6
US-09-909-207-2
; Sequence 2, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
FILING APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhelm F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: mat peptide
LOCATION: 1..663
FEATURE:
NAME/KEY: CDS
LOCATION: 1..663
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-909-207-2

Query Match 89.1%; Score 663; DB 9; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.4e-184;

Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CAAATCGTCACCGACAATTCATTCGGCAACACGATGGCTATGATTAATTTGGAAA 141
 Db 1 CAAATCGTCACCGACAATTCATTCGGCAACACGATGGCTATGATTAATTTGGAAA 60

QY 142 GATAGCGGTGCTCTGGGACAATGATTCCTCAATCATGGCGGTACGTTCAAGTGCCTCAATGG 201
 Db 61 GATAGCGGTGCTCTGGGACAATGATTCCTCAATCATGGCGGTACGTTCAAGTGCCTCAATGG 120

QY 202 AACATGTTAAACAATATATTCGTAAGTAAAGTAAATTAATCAATGAACACAAACACAC 261
 Db 121 AACATGTTAAACAATATATTCGTAAGTAAAGTAAATTAATCAATGAACACAAACACAC 180

QY 262 CAACAAGTTGTAACATGTCCTCAATCAATGTCCTCAATCAATGTCCTCAATCAATGTCCTCA 321
 Db 181 CAACAAGTTGTAACATGTCCTCAATCAATGTCCTCAATCAATGTCCTCAATCAATGTCCTCA 240

QY 322 TATTTATGCGTCTATGGTGGACTGTTGACCCCTCTTGTGCAATATATATTTGTCGACAGT 381
 Db 241 TATTTATGCGTCTATGGTGGACTGTTGACCCCTCTTGTGCAATATATATTTGTCGACAGT 300

QY 382 TGGGCAACTGGCGTCCACGAGGACCAAGCCCTAAGGGGACATCACTGTTGATGGAGGA 441
 Db 301 TGGGCAACTGGCGTCCACGAGGACCAAGCCCTAAGGGGACATCACTGTTGATGGAGGA 360

QY 442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCATTAAAGGGATTGCCACA 501
 Db 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCATTAAAGGGATTGCCACA 420

QY 502 TTAAACAATATTTGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCAATTTCTGTACGC 561
 Db 421 TTAAACAATATTTGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCAATTTCTGTACGC 480

QY 562 AACCACTTTAGAGCGTGGGAAACTTAGGATGAATATGGGAAATATGATGAAGTCGC 621
 Db 481 AACCACTTTAGAGCGTGGGAAACTTAGGATGAATATGGGAAATATGATGAAGTCGC 540

QY 622 CTACTGTAGAGGCTATCAAGTAGCGGAAGTGTATATGATATAGCAATACACTAGA 681
 Db 541 CTACTGTAGAGGCTATCAAGTAGCGGAAGTGTATATGATATAGCAATACACTAGA 600

QY 682 ATTAACGGTAACCTCTCTCACTATTATGATGATGACGAGACATACTTTGATAAATAAC 741
 Db 601 ATTAACGGTAACCTCTCTCACTATTATGATGATGACGAGACATACTTTGATAAATAAC 660

QY 742 AAT 744
 Db 661 AAT 663

RESULT 7

US-09-770-621-1
 ; Sequence 1, Application US/09770621
 ; Patent No.: US20010024815A1
 ; GENERAL INFORMATION:
 ; APPLICANT: M ntyl, Arja
 ; APPLICANT: Vehmaanper, Jari
 ; APPLICANT: Fagerstr m, Richard
 ; APPLICANT: Lantto, Raija
 ; APPLICANT: Paloheimo, Marja
 ; APPLICANT: Suominen, Pirkko
 ; APPLICANT: Lahtinen, Tarja
 ; TITLE OF INVENTION: Production and Secretion of Proteins of
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ; STREET: 1100 New York Ave., N.W. Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/770,621
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/590,563
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/332,412
 FILING DATE: 31-OCT-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/282,001
 FILING DATE: 29-JUL-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bugaisky, Lawrence B.
 REGISTRATION NUMBER: 35,086
 REFERENCE/DOCKET NUMBER: 1050.0340003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1375 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: No. US20010024815A1 Relevant
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 303..1334
 US-09-770-621-1

Query Match 16.0%; Score 119.4; DB 9; Length 1375;

Best Local Similarity 57.1%; Pred. No. 3.1e-24; Mismatches 176; Indels 3; Gaps 1;

Matches 238; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 279 GTCCATAAACTACGGAGCCAACTTCCAAACCAATGTAATGCGTATTTATGCGTCTATGG 338
 Db 608 GACCGTGACCTACAAACGCTCTTCAACCCGTCGGGTACGGCTACCTCAAGCTCTACGG 667

QY 339 TTGACCTGTTGACCTCTTGTGCAATATATATATGTCGACAGTTGGGGCAACTGGCGTCC 398
 Db 668 CTGGACCAGGAACCCGCTCGTCTGAGTACTACATCGTCGAGAGCTGGGGCACCTACCGGCC 727

QY 399 ACCAGGAGCAACGCTTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGA 458
 Db 728 CACCGG---CACCTACAAAGGGACCGGTCAACACGCGGGGACGTCACGACATCTACGA 784

QY 459 GACTCTTTAGAGTCAATCAACCCCTCCATTAAAGGGGATTCGCCACATTTAAACAATATTGGAG 518
 Db 785 GACCTGCGGTACAAACGCGCGTCCATCGAGGGCACCCGACCTTCCAGCAGTTCTGGAG 844

QY 519 TGTTGGAAGATCGAAACGCAAGTGGCAGCATTTCTGTGAGCAACACACTTTAGAGCGTG 578
 Db 845 CGTCCGGCAGCAGAAGCGGACCGAGCGGCACCATCACCATCGGCAACCACTTTCGACGCGTG 904

QY 579 GGAATACTTAGGGATGAATATGGGAAATGTATGAAGTCGCTTACTCTAGAGGCTA 638
 Db 905 GGCCCGCGCGCATGAACTGGGCGGACGACTACCATGATGCGGACCGAGGCTA 964

QY 639 TCAAGTAGCGGAAGTGTCTAATGTATATAGCAATATACACTAAGAAATTAACGGTAACCC 695
 Db 965 CCAGAGCAGCGGTAGTCTCCACCGTCTCCATCAGCGGGGTGGCAACCCCGGCAACCC 1021

RESULT 8


```

US-10-286-993-1
; Sequence 1, Application US/10286993
; Publication No. US20030148453A1
; GENERAL INFORMATION:
; APPLICANT: Mantyla, Arja
; APPLICANT: Paloheimo, Marja
; APPLICANT: Lantto, Raija
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Suominen, Pirko
; APPLICANT: Vehmaanjari, Jari
; TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
; TITLE OF INVENTION: Fungi
; FILE REFERENCE: 1716.0340004
; CURRENT APPLICATION NUMBER: US/10/286,993
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/120,804
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/FI97/00037
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: US 08/590,563
; PRIOR FILING DATE: 1996-01-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1375
; TYPE: DNA
; ORGANISM: Actinomadura flexuosa (Strain: DSM43186)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (303)...(1337)
; OTHER INFORMATION: Product= AM35 xylanase
; US-10-286-993-1

Query Match
Best Local Similarity 16.0%; Score 119.4; DB 15; Length 1375;
Matches 238; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 279 GTCCATAAACTACGGAGCCAACTTCCAAACAAATGATGCGTATTTATGCGTCTATGG 338
DB 608 GACCGTGACCTACACGCCCTCTTCAACCCGTCGGGTACCGGTACCTCACGCTCTACGG 667
QY 339 TTGGACTGTGACCTCTTGTGCAATATTATTTGTCGACAGTGTGGGCAACTGGCGTCC 398
DB 668 CTGGACAGCAACCCGCTGTCGAGTACTACATCGTCGAGAGCTGGGCACTTACCGGCC 727
QY 399 ACCAGGAGCAACCCCTAAGGGGACCATCACTGTTGATGGAGGAAACATATGATCTACGA 458
DB 728 CACCGG---CACCTACAGGGGACCGTCCACCGACGGGGGAACTGACATCTACGA 784
QY 459 GACTCTTAGAGTCAATCAACCTCCATTAAAGGGGATTCGACATTTTAAACAATTTGGAG 518
DB 785 GACCTGGCGGTACACACGGCGGTCATCGAGGGCACCCCGGACCTTCCAGCAGTTCTGGAG 844
QY 519 TGTTCGAAGATCGAAAGCAGAGTGGCAGGATTTCTGTGACGAAACCACTTTAGACGCTG 578
DB 845 CGTCCGCGCAGCAGAGCGGACCGACCATCACCATCGGCAACCACTTGCACGCCCTG 904
QY 579 GGAACACTTAGGATGAATATGGGAAATGATGAAGTCGCGCTTACTGTAGAGGCTA 638
DB 905 GGCCCGCGCGCATGAACTGGGCGCCACGACTACCATGATGATGGGACCGAGGCTA 964
QY 639 TCAAAGTAGCGGAGTGTCTAATGTATATATGATCAATACATTAAGAAATTAACGGTAAACC 695
DB 965 CCAGAGCAGCGGTAGTCTCCACCGTCTCCATCAGCGGGGTGGCAACCCCGGCAACCC 1021

RESULT 9
US-10-307-441-39
; Sequence 39, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.

US-10-286-993-1
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Trx
; US-10-307-441-39

Query Match
Best Local Similarity 15.5%; Score 115.2; DB 15; Length 596;
Matches 226; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

QY 274 AACATGTCCATAAACTACGGAGCCAACTTCCAAACAAATGATGCGTATTTATGCGTC 333
DB 191 AATAAGGTGATCAACTTCTCTGGATCTTATATCCGATGGGAATTCATCTTAAGCGTC 250
QY 334 TATGTTTGGACTGTTGACCCCTTTCGAAATATATATTTGTCGACAGTGTGGGCAACTGG 393
DB 251 TATGCTGGTCTAGAAACCCACTGATTGAATATTAATTCGAAAAATTCGGTACCTAC 310
QY 394 CGTCC---ACCAGGAGCAACGCCCTAAGGGGACCATCACTGTTGATGGAGGAAACATATGAT 450
DB 311 AATCCGAGTACCGGCGCCCAAAATTTAGCGGAAGTCACTAGTAGGATTCGCTATATGAT 370
QY 451 ATCTACGAGACTCTTTAGAGTCAATCAACCTCCATTAAAGGGGATTCGCCACATTTAAACAA 510
DB 371 ATCTACGATCCCAACCGGTTTATCAGCCATGATTCATTTGAAACCGCCACCTTTATCAG 430
QY 511 TATTTGGAGTGTTCGAAGATTCGAAACCGCAGAGTGGCAGGATTTCTGTGACGAAACCACTTT 570
DB 431 TACTGGAGTGTTCGAGCTAATCATCGGAGCTCCGGTTCGGTTAAATCTCGAATCACTTT 490
QY 571 AGAGCTGGGAAACTTAGGATGATATGGGAAATGATGAGGAAATGATGAGGCTTACTGTA 630
DB 491 AATGATGGGCAACGCAAGGGTTAACCCCTAGGTACAATGGATTATCAAAATCGTAGCGGTG 550
QY 631 GAAGGCTATCAAAAGTAGCGGAAGTGTCTAATGT 662
DB 551 GAAGGCTACTTCTCGAGTGGTTCGCTAGTAT 582

RESULT 10
US-10-213-990-71
; Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Aspergillus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(942)
US-10-213-990-71

Query Match      15.0%; Score 111.4; DB 14; Length 942;
Best Local Similarity 57.0%; Pred. No. 5.9e-22;
Matches 224; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

Qy 263 AACAGTTGGTAACATGTCATAAAGTACGGAGCAACTTCCAAACCAAAATGGTAATGGT 322
Db 257 ATCCAGGAGTGACCATGACATACCTTCTCTGGCAGCTTCAATCTCTCCGGAAATGCTT 316
Qy 323 ATTTATGCGTCTATGGTGGAGTGTGACCTCTTGTGCAATATATATTTGTGCACAGTT 382
Db 317 ACCTGTCCGTGTATGGATGGAGTACCAACCCCTAGTCGAATACTACATCTCCAGAACT 376
Qy 383 GGGCA---ACTGGGGTCCACAGGAGCAACGCTTAAGGGGACCATCACTGTTCATGGAG 439
Db 377 ATGGCAGTTAATCTGGCTGGGCATGACGCAAGGGCACCGTCAACGAGCGATGGAT 436
Qy 440 GAACATATGATATACAGAGACTTTAGAGTCAATCAACCTCCATTAAAGGGGATTCGA 499
Db 437 CCACCTACGACATCTATGAGCACCACAAAGGTCAACAGCCTTCGATCTGGCAGCGCA 496
Qy 500 CATTTAAACATATTTGGAGTGTTCGAAGATCGAAACGACAGTGGCAGCATTTCTGTCA 559
Db 497 CTTTCAACCAATACTGGTCCATCCGCCAAACAAAGCGATCCAGCGGCACAGTCAACCCG 556
Qy 560 GCAACCACTTTAGAGCGTGGGAAACTTTAGGATGAATATGGGAAATGATGAAGTCG 619
Db 557 CGAATCACTTCAAGCCTGGGCTAGTCTGGGATGAACCTGGTACCCATACATATCAGA 616
Qy 620 CGCTTACTGTAGAAGGCTATCAAGTAGTCGGAA 652
Db 617 TTGTTTCCACTGAGGATATGAGAGCGCGTA 649

RESULT 11
US-10-213-990-70
; Sequence 70, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-70

Query Match      14.8%; Score 110; DB 14; Length 1002;
Best Local Similarity 57.8%; Pred. No. 1.6e-21;
Matches 216; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

Qy 282 CATAAATACGGAGCAACTTCCAAACCAAAATGGTAATGGTATTTATCGCTATGGTTG 341
Db 336 CATTACCTTCTCTGGCAGCTTCAATCTCTCCGAAATGCTTACCTGTCCGTGTATGGATG 395
Qy 342 GACTGTTGACCTCTTGTGCAATATATATTTGTTCGACAGTTGGGCA---ACTGGCGTCC 398
Db 396 GACTACCAACCCCTTAGTCGAATACTACATCTCCAGAACTATGCGAGTTCAATCTCTGG 455
Qy 399 ACCAGGACCAACCCCTTAAGGGGACCATCACTGTTGATGGAGCAATATGATATCTACGA 458
```

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Db 456 CTGGGATGACGCAAGGGGACCGTCAACAGGATGGATCCACCTACGACATCATGA 515
Qy 459 GACTCTTAGAGTCAATCAACCTCCATTAAAGGGGATTCGACATTTAAACAATATTGGAG 518
Db 516 GCACCAACAGGTCAACAGGCTTCGATCGTCGGCAGCGCCACCTTCAACCAATACTGCTC 575
Qy 519 TGTTGGAAGATCGAAACGACGAGTGGCAGATTTCTGTGAGCAACACCTTTAGAGCGTG 578
Db 576 CATCCGCCAAACAAAGCGATCCAGCGGCACAGTCAACCCGCGAATCACTTCAAGGCTG 635
Qy 579 GMAAACTTAGGGATGAATATGGGAAATGTATGAAGTGGCGCTTACTGTAGAGGCTA 638
Db 636 GGCTAGTCTGGGATGAACCTGGTACCCATACTATCAGATTGTTTCCACTGAGGGATA 695
Qy 639 TCAAAGTAGCGGAA 652
Db 696 TGAGAGCAGCGGTA 709

RESULT 12
US-10-213-990-68
; Sequence 68, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; NAME/KEY: CDS
; LOCATION: (1)...(705)
US-10-213-990-68

Query Match      14.6%; Score 108.8; DB 14; Length 705;
Best Local Similarity 51.9%; Pred. No. 3e-21;
Matches 298; Conservative 0; Mismatches 267; Indels 9; Gaps 2;

Qy 87 CGTCAACGACAAATTCCTATTCGCAACCAACGATGGCTATGATTAATGAAATTTTGGAAAGTAG 146
Db 120 CGGCACCCCAAGCTCCACCGCTGGGAACACGGCTACTACTCTCTTCTGGACTGATGG 179
Qy 147 CGGTGGCTCTGGGACAATGATTTCAATCATATGGCGGTACGTTCAATGAGTCCCAATGAAACA 206
Db 180 CGCGCGGACGTGACCTACACCAATGGCGCGGTGGCTGCTACTCCGTCAACTGGAGAA 239
Qy 207 TGTTAACACATATATTCGTAAAGGTAAATAATTCATGAACACACCAACACACACCAACA 266
Db 240 CGTGGCAACTTTGTCTGGTGGAAAGGGC-----TGGAAACCTTGGAGCGGTAGGTACCG 293
Qy 267 AGTTGGTAACATGTCCTAAACTACGGAGGCAACTTCCAAACCAATGGTATGCGTATTT 326
Db 294 AGCTTTAGTAGAACCATCACTACGGAGGAGCTTCAACCCCGCGCAATGGCTACCT 353
Qy 327 ATGCGTCTATGGTGGAGTGTGACCTCTTGTGCAATATATATTTGTGCAAGTGGGG 386
Db 354 GGCTGTCTACGGCTGGACCAACCCCTTGAATGAGTACTACCTGTTGAGTGGTATGG 413
Qy 387 CA---ACTGGCGTCCACCGAGGACCAACGCTTAAGGGGACCATCACTGTTGATGAGGAAAC 443
Db 414 TACATACACCCCGGAGCGCGGTACTCTTCAGGGGCACTGTCTCAACCCGACGGTGGCAC 473
```

QY 444 ATATGATATCTAGGAGACTCTTAGAGTCAATCAACCCCTCCATTAGGGGATGGCCACATT 503
DB 474 TTACAACATCTACACGGCGTTTCGTACAAATGCTCCCTCCATCGAAGGACCAAGACCTT 533
QY 504 TAAACAATATTGGAGTGTTCGAAGATCGAAACGACAGTAGTGGCAGATTTCTGTGAGCAA 563
DB 534 CACCCAGTACTGCTGTGCGGACCTCCAGGCTACCGGGGCACTGTCCACCATGGCCAA 593
QY 564 CCATTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGGGGAATAATGTATGAAGTCCGCGT 623
DB 594 CCATCTCAACGCGCTGGAGCAGACTGGGCATGAACCTGGGAACTCACAACCTACAGATTGT 653
QY 624 TACTGTAGAGGCTATCAAGTAGCGGAGTGCT 657
DB 654 CGCCACTGAGGGTTACCGAGCAGCGGATCTGCT 687

RESULT 13

US-10-299-393-1
; Sequence 1, Application US/10299393
; Publication No. US20030108642A1
; GENERAL INFORMATION:
; APPLICANT: Sabatier, Alain
; APPLICANT: Fish, Neville Marshall
; APPLICANT: Haigh, Nigel Paterson
; TITLE OF INVENTION: PENICILLIUM FUNICULOSUM STRAIN USEFUL
; FILE REFERENCE: A32917-PCT-USA-1 (072667.0183)
; CURRENT APPLICATION NUMBER: US/10/299,393
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 09/462,246
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: EPO 9801161.5
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2898
; TYPE: DNA
; ORGANISM: Penicillium funiculosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1317)...(1589)
; NAME/KEY: intron
; LOCATION: (1590)...(1642)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1644)...(2042)
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (570)...(576)
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (724)...(730)
; US-10-299-393-1

Query Match 14.2%; Score 106; DB 15; Length 2898;
Best Local Similarity 56.5%; Pred. No. 4.1e-20;
Matches 218; Conservative 0; Mismatches 165; Indels 3; Gaps 1;
QY 276 CATGTCCATAAATACGAGCCAACTTCCAAACAAATGGTAATTTATGCGTCTA 335
DB 1640 CAGGACTGTACGTACTCAGGAGAAATTAACCCCTCTGGAAACGCTTTATTTGGCTGTCTA 1699
QY 336 TGGTTGACGTGTGACCCCTTGTTCGAATATTATATGTTCGACAGTTGGGGCACTGGCG 395
DB 1700 CGGGTGACAACACAGATCCTCTTGTTCGAATATTACTATCATCCTGGAGTCTTACGGCACTATAA 1759
QY 396 TCCACCA---GGAGCAACGCTTAAGGGGACCATCCTGTTGTGGAGGAAACATATGATAT 452
DB 1760 CCATCATCTGGACTTACTTCACTTGGCCAGGTCACCTAGCGATGGTGGCACCTACGATAT 1819

QY 453 CTACGAGACTCTTAGAGTCAATCAACCTCCATTAAAGGGGATGGCCACATTAAACAATA 512
DB 1820 CTACTCAACCCAGCGTGTCAACCAAGCCTTCCATTGAGGGAACCTCCACCTTCAACCACTA 1879
QY 513 TTGAGTGTTCGAAGATCGAAACGACGAGTGGGACGATTTCTGTGACGACCACTTTAG 572
DB 1880 CTGGTCACTTCCGACCGAGAACGAGTCCGGCGGAACCTGTCCACGCGGCAACCACTTTGC 1939
QY 573 AGCTTGGGAAAACCTTAGGGATGAATATGGGGAATAATGTATGAAGTCCGCGCTTACTGTGTA 632
DB 1940 AGCATGGGAAGCAGCTTGGACTTGAATGGGCACTTATAACTATATGATTTGTGTCACCGA 1999
QY 633 AGGCTATCAAAAGTAGCGGAAGTGCTA 658
DB 2000 AGGCTACGAGAGCAGTGGCTCTAGTA 2025

RESULT 14

US-10-213-990-64
; Sequence 64, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 712
; TYPE: DNA
; ORGANISM: Aspergillus
; US-10-213-990-64

Query Match 14.1%; Score 104.8; DB 14; Length 712;
Best Local Similarity 55.8%; Pred. No. 4.5e-20;
Matches 221; Conservative 0; Mismatches 172; Indels 3; Gaps 1;
QY 270 TGGTAACATGTCCATAAACTACGGAGCCAACTTCCAAACCAATGGTAATGCGTATTATG 329
DB 304 TGGATTGAGCGGTCACCTACAGCGGCTCTCGGACGACGCGGAAACGGCTACCTC 363
QY 330 CGTCTATGTTGGACTGTTGACCCCTTGTTCGAATATTATATGTTCGACAGTTGGGGCAA 389
DB 364 CGTGTACGGCTGGACGACCAGTCCGCTGGTTCGAATTCATCTCGTGGAGATTACGGCTC 423
QY 390 CTGGCGTCCACCA---GGAGCAACGCTTAAGGGACCATCATCTGTTGATGGGGAACATA 446
DB 424 CTATGACCCCTCCACGGGAGCCACCATCTCGGACCCGTCGAGAGCGAGCGGGGCCACGTA 483
QY 447 TGNATCTACGAGACTCTTTAGAGTCAATCAACCTCCATTAAGGGGATTTGCCACATTTAA 506
DB 484 CAACTCTTACAAGACGACCGGACGAGATGCGGCGTCCATCCAGGCGACCGCTACTTTGA 543
QY 507 ACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTAGCAACCA 566
DB 544 CCAGTACTGTTCGGTTTCGGACTTCGCACCGCGCAGAGTGGAACCTGTGACGACGAGAACCA 603
QY 567 CTTTAGAGCGTGGGAAAACCTTAGGGATGAATATGGGGAATAATGTATGAAGTCCGCGCTAC 626
DB 604 CTTTGTGCTGGAGAAATCGCGGCTCTGCAATTTGGGGAACCTTTGACTATATGATTGTTGC 663
QY 627 TGTGAAGGCTATCAAGTAGCGGAGTGTCTATGT 662
DB 664 GACGGAGGGGTACCGAGCAGCGGCTCTGCTACTAT 699

RESULT 15

US-10-213-990-65
; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213.990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(666)
US-10-213-990-65

Query Match 13.9%; Score 103.6; DB 14; Length 666;
Best Local Similarity 56.3%; Pred. No. 9.8e-20;
Matches 215; Conservative 0; Mismatches 164; Indels 3; Gaps 1;
QY 284 TAACTACGGAGCCAACTTCCAAATGGTAATGCTATTTATGCTCTATGTTGGA 343
DB |||||
QY 272 TCACCTACAGCGGCTCTCGGAGACGAGCGGAACTCTCTCGGTGTACGGCTGA 331
DB |||||
QY 344 CTGTTGACCTCTTCTGCAATATTATTTGCGACAGTTGGGCAACTGGCGTCCACCA - 402
DB |||||
QY 332 CGACAGTCCGCTGTGCGAATTTCTACATCGTGGAGAGTTACGGCTCTTATGACCCCTCA 391
DB |||||
QY 403 --GGAGCAACGCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGAGA 460
DB |||||
QY 392 CGGAGGCCACCCATCTCGGCACCGTCGAGAGCGAGCGGGGCCACGTACAACTCTACAAGA 451
DB |||||
QY 461 CTCCTTAGAGTCAATCAACCTCCATTAAGGGGATTCACATTTAAACAATATTGGAGTG 520
DB |||||
QY 452 CGACGCGGACGAATGCGCCGCTCCATCCAGGCGACGGCTACTTTTGACCACTACTGGTCGG 511
DB |||||
QY 521 TTCGAAGATCGAAACGACAGTGGCAGATTTCTGTGAGCAACCACTTTAGAGCGTGGG 580
DB |||||
QY 512 TTCGACTTTCGACCGGAGAGTGGAACTGTGACGACGAAGAACCACTTTGATCGGTGA 571
DB |||||
QY 581 AAACTTAGGATGAATATGGGAAATGTATGAGTCGCGCTTACTGTAGAAGGCTATC 640
DB |||||
QY 572 GAAATGCGGGTCTGCAATTTGGGAACTTTGACTATATGTTGTCGACGGAGGGGTACC 631
DB |||||
QY 641 AAAGTAGCGGAAGTCTAATGT 662
DB |||||
QY 632 AGACAGCGGCTCTGCTACTAT 653
DB |||||

Search completed: November 11, 2004, 02:08:23
Job time : 476.684 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 10, 2004, 16:24:32 ; Search time 3225.17 Seconds
(without alignment)
8406.125 Million cell updates/sec

Title: US-09-909-207-4
Perfect score: 744
Sequence: 1 ATGACACAAAGAAATTGAC.....TAACCTTTGGATATAAAACAAT 744

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98.6	13.3	618	7	CF472462 RTDS1_9_C
2	93	12.5	728	7	CN132941 OX1_9_D10
3	93	12.5	772	7	CN133022 OX1_9_D10
4	91.8	12.3	744	7	CF867983 trico13xe
5	91.8	12.3	799	6	CB898036 trico13xe
6	86.6	11.6	738	6	CD464145 ETH1_48_B
7	83.4	11.2	921	6	CD458837 Fg08_04B1
8	82.8	11.1	603	8	AQ160513 mgxb0006C
9	82.2	11.0	670	8	AQ447125 mgxb0005C
10	82.2	11.0	720	8	AQ361561 mgxb0004B
11	82.2	11.0	750	8	AQ160254 mgxb0003L
12	81.6	11.0	786	8	AQ325248 mgxb0021M
13	81.4	10.9	583	8	AQ399120 mgxb0001B
14	76.6	10.3	561	8	AQ396475 mgxb0010M
15	76.4	10.3	617	1	AJ638869 AJ638869
16	76.2	10.2	768	7	CF881056 trico83xj
17	76.2	10.2	822	6	CB907827 trico83xj
18	74.6	10.0	753	8	AQ448084 mgxb0016B
19	74.4	10.0	418	8	AQ398756 mgxb0005L
20	71.8	9.7	746	6	CB901964 trico28xi
21	71.8	9.7	746	7	CF871731 trico28xi
22	69.8	9.4	520	5	BQ165950 WHE0821-0
23	66.2	8.9	561	5	BQ471960 HV04A02r
24	63.2	8.5	473	6	CD464005 ETH1_48_B

C 25	60.4	8.1	483	5	BQ664593	HV04A02u
C 26	53.6	7.2	646	8	AQ449078	mgxb0022H
C 27	51.6	6.9	493	7	CO135442	EST830113
28	49.4	6.6	490	2	BF200865	WHE0821-0
29	49.4	6.6	532	7	BM134812	WHE0452_F
30	48.4	6.5	532	7	CN008236	WHE2638_H
31	47.8	6.4	743	7	CF865758	trico0032B
32	47.8	6.4	802	6	CB895680	trico0032B
C 33	46.6	6.3	503	5	BQ166480	WHE0861_D
C 34	46.6	6.3	1582	9	CF820765	SSH_RfPDI
35	46.4	6.2	456	1	AJ637947	AJ637947
36	45.2	6.1	587	6	CD033274	mgmco12KD
37	44.8	6.0	614	6	CA278095	SCFSD203
38	41.6	5.6	488	4	BM135798	WHE2624_C
39	41.6	5.6	591	4	BJ375180	BJ375180
C 40	41.4	5.6	1201	9	CNS007JU	Drosophila
41	40.8	5.5	622	4	BJ401024	BJ401024
42	40.8	5.5	642	4	BJ402691	BJ402691
43	40.8	5.5	655	4	BJ372089	BJ372089
44	40.8	5.5	782	8	BH066221	RPCI-24-2
45	40.6	5.5	474	4	BJ398920	BJ398920

ALIGNMENTS

RESULT 1
CF472462
LOCUS
DEFINITION
RTDS1_9_C03.g1_A015 Drought-stressed loblolly pine roots DS1 Pinus taeda cDNA clone RTDS1_9_C03_A015 5', mRNA sequence.
ACCESSION
CF472462
VERSION
CF472462.1
KEYWORDS
EST.
SOURCE
Pinus taeda (loblolly pine)
ORGANISM
Pinus taeda
REFERENCE
1 (bases 1 to 618)
AUTHORS
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.
TITLE
An EST database from drought-stressed loblolly pine (Pinus taeda) roots
JOURNAL
Unpublished (2003)
COMMENT
Other_ESTs: RTDS1_9_C03_b1_A015
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@cuga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JFNREV (CAGGAACAGCTATGACC).

FEATURES
source
1..618
Location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CLONES"
/db_xref="taxon:3352"
/clone="RTDS1_9_C03_A015"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Drought-stressed loblolly pine roots DS1"
/notes="vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from drought-stressed loblolly pine (Pinus taeda) roots. Water was withheld from

ramet clones until predawn needle water potential reached -1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 13.3%; Score 98.6; DB 7; Length 618;
Best Local Similarity 57.4%; Pred. No. 9.6e-17;
Matches 198; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 263 AACAGTGGTAACATGTCCTAATACCTAGGAGCACTTCCACCAATGTAATCGGT 322
Db 254 ATCCAGGTAGTGGCAGGACATCACTTCTCCGGTACCTTCCAGCCCGCAGAGAACGCT 313
QY 323 ATTTATGCGTCTATGTTGGAGTGTGACCTCTTGTGCAATATATATATGTCACAGTT 382
Db 314 ATCTTGGCGTCTACGGCTGGACCCAGCCCTCTGTGATGATATACATTTCTCGAAGCT 373
QY 383 GGGGCACTGGCGTCC---ACCAGGAGCAACGCTTAAGGGACCATCTGTTGATGGAG 439
Db 374 ATGGACCTACAACTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 433
QY 440 GAACATATGATCTACGAGACTCTTAGATCAATCAACCTCCATTAAAGGGATTGCCA 499
Db 434 CGACCTATGATATCTATGAGCAGCAGCAAGTCAACCGCTCTATCGTGGCAGCGGA 493
QY 500 CATTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTCA 559
Db 494 CTTTCAACCATATCTGTTCCATCTCGTCAGACGAGCGTCCAGCGGAATCTCACTACAG 553
QY 560 GCAACCATTTAGCGGTGGGAAACCTTAGGGATGAATATGGGA 604
Db 554 CGAACCAATTTCAACGCTGGGTGCTTGGGCATGAACCTGGGA 598

RESULT 2

CN132941
LOCUS
DEFINITION
XO1_9_D10_b1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA clone XO1_9_D10_A002 3', mRNA sequence.
CN132941
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
AUTHORS
Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H.
TITLE
JOURNAL
COMMENT
An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003)
Other ESTs: XO1_9_D10_g1_A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug3-14 (TAGTCTAGCGCCGCGACC)
POLYA=Yes.

FEATURES

Location/Qualifiers

source

1. .728
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="OX1_9_D10_A002"
/lab_host="DH10B-Ti phage-resistant E. coli"
/clone_lib="Oxidatively-stressed leaves and roots"
/notes="Organ: Leaf and Root; Vector: pME18S-FL3; Site: 1; XhoI; Site: 2; XhoI; The library was prepared from polyA+ RNA from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were misted with 10 uM methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 12.5%; Score 93; DB 7; Length 728;
Best Local Similarity 53.9%; Pred. No. 3.9e-15;
Matches 214; Conservative 0; Mismatches 180; Indels 3; Gaps 1;
QY 281 CCATAACTACGAGCCCACTTCCAAACCAATGTAATGTAATGTAATGTAATGTAATGTA 340
Db 101 CCATCAACTATGGCGTCTTTTCAGCCCTCAGGGTAACGGCTACCTCTGGCTCTACGGCT 160
QY 341 GGACTGTTGACCCCTCTTGTGCAATATTTATTTGTCGACAGTTGGGCA---ACTGGCGTC 397
Db 161 GGACTCGACCCCTCTCGTTGAGTACTACGTCATCGAGAACTACGGCACTTACAACCGCTG 220
QY 398 CACAGAGCAACGCTTAAGGGAGCACTACTGTTGATGAGGAACATATGATATCTACG 457
Db 221 GCTCTGTCGACGACCAAGGGCACCGCTCTACAACGCGGACACCTAGATCTCTACC 280
QY 458 AGACTCTTAGAGTCAATCAACCTCCATTAAAGGGATTGCCACATTTAAACAATATTGGA 517
Db 281 AGACACCCGCTACACAGCCCTCTATCGACGCCAACAGACCTTCAACAGTACTGGG 340
QY 518 GTGTTGGAAGATCGAAACGACGAGTGGCAGATTTCTGTGAGCAACCATTTAGACGCT 577
Db 341 CCATCCCGCCCAACAAGCGCAGCAGCGCGCGCTCAACATGACAGACTATCTTCAATGCTT 400
QY 578 GGGAAACTTAGGATCAATATGGGAAATGATGAAGTCGCGCTTACTGTAGAAGGCT 637
Db 401 GGGCTAAGCTGGTATGAGACTTTGGAACCACTACTACCAATCTCTGGCTACCGAGGAT 460
QY 638 ATCAAACTAGCGGAAGTGTAAATGATATATAGCAATAC 674
Db 461 ACCAGACAGTGGATCTTCTTCTATCTATGTCCAGAC 497

RESULT 3

CN133022
LOCUS
DEFINITION
XO1_9_D10_g1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA clone XO1_9_D10_A002 5', mRNA sequence.
CN133022
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
AUTHORS
Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H.
TITLE
JOURNAL
COMMENT
An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003)
Other ESTs: GI:45963542
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug3-14 (TAGTCTAGCGCCGCGACC)
POLYA=Yes.

COMMENT Other ESTs: OX1_9_D10.bi.A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGGC) .

FEATURES
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Location/Qualifiers
/organism="Sorghum bicolor"
/mol_type="mRNA"
/culturvar="BTx623"
/db_xref="taxon:4558"
/clone="OX1_9_D10.A002"
/lab_host="DH10B-Ti phage-resistant E. coli"
/clone_lib="Oxidatively-stressed leaves and roots"
/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site 1:
XhoI; Site 2: XhoI; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 mM methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all
tissue pooled. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites of the
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
insert."

ORIGIN
Query Match 12.5%; Score 93; DB 7; Length 772;
Best Local Similarity 53.9%; Pred. No. 3.9e-15;
Matches 214; Conservative 0; Mismatches 180; Indels 3; Gaps 1;
QY 281 CCATAAAGTACGAGGCAACTTCCAAACCAATGGTAATGCGTATTTATCGCTATGTT 340
Db |||||
324 CCATCAACTATGCGGTTCTTTCAGGCCCTCAGGTAACGGCTACCTCTGCGTCTACGGCT 383
QY |||||
341 GGACTGTTGACCTCTTGTGCAATATATATTGTCACAGTTGGGCA---ACTGGCGTC 397
Db |||||
384 GGACTCGCAGCCCTCTCGTGTAGTACTACGTCTATCGAGAACTACGGCACTTACACCCCTG 443
QY |||||
398 CACCAGGAGCAACGCTTAGGGGACCATCACTTGTGAGGAGCAATATGATATCTACG 457
Db |||||
444 GCTCTGCTGCCAGCAGCAGGCAACCGTCTAACAGCGGCACTACGATCTCTACC 503
QY |||||
458 AGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGCGCAATTAACAATATGGA 517
Db |||||
504 AGACCCCGCTACACCCAGCCCTCTATCGAGCGCAACAGACCTTCAACACGACTGGG 563
QY |||||
518 GTGTTGGAAGATCGAAACGACAGTGGCAGGATTTCTGTACGACCAACCTTTAGAGCGT 577
Db |||||
564 CCATCGCGCCGAACAGCGCAGCGCGCGCGCTCAACATGCAAGATCTCTTCAATGCTT 623
QY |||||
578 GCGAAACTTAGGGATGAATATGGGAAATGATGAGTGGCGCTTACTGTAGAAGGCT 637
Db |||||
624 GGCTAACCGCTGTATGAGACTTGGAAAACCACTACTACAGATCTCTGGCTACCGAGGAT 683
QY |||||
638 ATCAAAGTACGGAAGTGTGTAATGTATATAGCAATAC 674
Db |||||
684 ACCAGAGCAGTGGATCTTCTTCTATCTATGTGCCAGAC 720

RESULT 4
CF867983 744 bp mRNA linear EST 31-OCT-2003
LOCUS tricol3xe09.bl T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina cDNA clone tricol3xe09, mRNA sequence.
ACCESSION CF867983
VERSION 1
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 744)
AUTHORS Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,
Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K.,
Ward, M. and Dean, R.A.
TITLE Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: LR-F1 primer.
Location/Qualifiers
1..744
source
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clones="tricol3xe09"
/dev stages="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
2003"
/note="Vector: pREP3V, Site 1: Not 1/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Query Match 12.3%; Score 91.8; DB 7; Length 744;
Best Local Similarity 55.0%; Pred. No. 8.5e-15;
Matches 202; Conservative 0; Mismatches 162; Indels 3; Gaps 1;
QY 274 AACATGTCCTATAAACTACGGAGCCAACTTCCAAACCAATGGTAATGCGTATTTATGCGTC 333
Db |||||
353 AACAGGTATCACTTCTCGGGCAGCTACACCCCAACGGCAACAGCTACCTCTCCGTG 412
QY |||||
334 TATGTTGAGCTGTGACCTCTTGTGCAATATATATTTGTGACAGTTGGGGCACTGG 393
Db |||||
413 TACGGCTGGTCCCGCAACCCCTGTATCGAGTACTACATCGTCGAGAACTTTGGCACCTAC 472
QY |||||
394 CGTCCACCA---GGAGCAACGCTTAAGGGACCATCACTGTTGATGGAGCAATATGAT 450
Db |||||
473 AACCCGTCACGGGCGCCACCAAGTGGGCGAGGTCACTCCGACGGCAGCGTCTACGAC 532
QY |||||
451 ATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACATTTAAACAA 510
Db |||||
533 ATTTACCGCAGCAGCGCGCTCAACAGCGCTCCATCATCGGCACCGCCACCTTTTACCAG 592
QY |||||
511 TATTGGAGTGTTCGAAGATCGAAACGACAGTGGCAGATTTTGTGTGACGACCACTTTT 570
Db |||||
593 TACTGTGCTCGCGCGCAACCCAGCTCGAGCGGCTCGTCAACACACGCGCAACCACTTTC 652
QY |||||
571 AGAGCGTGGAAAACTTAGGATGATATATGGGAAATATGATGAGTTCGCGCTTACTGTA 630
Db |||||
653 AACGGGTGGGCTCAGCAAGGCTCTGACGCTCGGGAGCGATGATTAACAGATTGTTGCCGTG 712
QY |||||
631 GAAGGCT 637

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Db      713 GGAGGGT 719

RESULT 5
CB898036
LOCUS
DEFINITION
    tricol13xe09 T. reesei mycelial culture, Version 3 april Hypocrea EST 02-JUL-2003
ACCESSION
CB898036
VERSION
CB898036.1 GI:30112694
KEYWORDS
EST.
SOURCE
Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE
1 (bases 1 to 799)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
22803314
PUBMED
12788920
COMMENT
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
1..799
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tricol13xe09"
/dev_stage="mycelia"
/clone_lib="T. reesei mycelial culture, Version 3 april"
/notes="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

FEATURES
source
1..738
Location/Qualifiers
1..738
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="ETH1_48_B06_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Ethylene-treated seedlings"
/notes="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
material from both time points was combined prior to RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites is CACTGTGTC,
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTC,
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
insert."

ORIGIN
Query Match 12.3%; Score 91.8; DB 6; Length 799;
Best Local Similarity 55.0%; Pred. NO. 8.7e-15;
Matches 202; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

QY 274 AACATGTCNTAAACTACGAGCCCACTTCCAAACCAATGTAATGCGTATTATGCGTC 333
DB 408 AACAAAGGTCATCACTTCTCGGGCAGCTACACCCCAACGGAACAGTACTCTTCGCTG 467
QY 334 TATGCTGGACGTGTGACCTCTTCTGCAATATTATTTGTCGACAGTTGGGCAACTGG 393
DB 468 TACGCTGTGTCGGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACTAC 527
QY 394 CGTCCACCA---GGAGCAACGCTTAAGGGGACCAATCACTGTTGATGGAGGAACATATGAT 450
DB 528 AACCGGTCCACGGGCGCCACCAAGCTGGCGAGGTCACTCCGACGGCAGCGTCTACGAC 587
QY 451 ATCTACGAGACTTTAGAGTCAATCAACCTCCATTAAGGGATGCGACATTTAAACAA 510
DB 588 ATTTACCGACGACGCGGTCAACGACGCGTCCATCATCGGACCGCCACCTTTTACCAG 647
QY 511 TATTGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTGTCAGCAACCACTTT 570
DB 648 TACTGTCGTCGCGCGCAACCAACGCTCGTACGAGCGCTCGTCAACACGGGACCACTTC 707
QY 571 AGAGCGTGGGAAAACCTTAGGATGATATGAGGGAATAATGTAAGTGCAGCTTACTGTA 630
DB 708 AACCGTGGGCTCAGCAAGGCGCTGACGCTCGGACGATGGATTACCAATGTTGCGCTG 767

```

```

QY 631 GAAGGCT 637
DB 768 GGAGGGT 774.

RESULT 6
CD464145
LOCUS
DEFINITION
    ETH1_48_B06_g1_A002 Ethylene-treated seedlings Sorghum bicolor cDNA
    clone ETH1_48_B06_A002 5', mRNA sequence.
ACCESSION
CD464145
VERSION
CD464145.1 GI:31385413
KEYWORDS
EST.
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 738)
Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,
Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R.,
Chua Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P.,
Olaseinde, O., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
(ACC)-treated seedlings
Unpublished (2003)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sunio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).
Location/Qualifiers
1..738
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="ETH1_48_B06_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Ethylene-treated seedlings"
/notes="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
material from both time points was combined prior to RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites is CACTGTGTC,
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTC,
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
insert."

ORIGIN
Query Match 11.6%; Score 86.6; DB 6; Length 738;
Best Local Similarity 53.5%; Pred. No. 2.6e-13;
Matches 204; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY 281 CCATAAATCTCGGAGCCCACTTCCAAACCAATGTAATGCGTATTATGCTCTATGTT 340

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Db 345 CCATCAAGTACTCTGTTACTTACAACTCAACGGAACAGCTACCTCGCTGTTTACGGAT 404
 QY 341 GGACTGTTGACCTCTGTCGAATATATATGTCGACAGTTGGGGCACTGGCGTCCAC 400
 Db 405 GGACTCAGAACCTCTCATCGAGTACTACATCGTTGAGAACTTCGGCACTTACAAACCCCT 464
 QY 401 CA---GGAGCAACGCTTAAGGGACCACTGTTGATGGAGAACATATATATCTACG 457
 Db 465 CTTCCGGCGGCGCAGAAAGGCTAGGCTCAGTCTGTTGACGATCTGTTACGATCTACG 524
 QY 458 AGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTGCCACATTTAAACAATATGGA 517
 Db 525 TCAGCAACCGTGTCAACGCCCTCCATTTAGGGTAAACAAGACCTTTTTCAGCAGTCTGGT 584
 QY 518 GTGTTGGAAGATGGAACGACGAGTGGCAAGATTTCTGTGACGAACACATTTAGAGCGT 577
 Db 585 CTGTTGCGAGCAACAAAGCGATCCAGCGGATCCGTCACACACCGGTCTCACTTCCAGGCT 644
 QY 578 GGGAAACTTAGGGATGATATATGGGGAATGATGAAGTCGCTTACTGTAGAGGCT 637
 Db 645 GGAATAATGTCGGCTCAACCTTTGGTAACCAACATATCAGATCTTGTGTTGAGGCT 704
 QY 638 ATCAAAGTAGCGAGTGTCTA 658
 Db 705 ACTACAGCTCTGGCTTGCCA 725

RESULT 7
 CD458837 921 bp mRNA linear EST 14-JUN-2004
 LOCUS Fg08_04b10_A Fg08_AAPC_ECORC_Fusarium_graminearum_complex_substrate
 DEFINITION Gibberella zeae cDNA clone Fg08_04b10, mRNA sequence.
 CD458837
 CD458837.1 GI:31373577

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Gibberella zeae
 Gibberella zeae
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 1 (bases 1 to 921)
 Watson, R.J., Heyes, R., Chapados, J., Couroux, P., Harris, L.J.,
 Hattori, J., Lacroix, C., Quillet, T., Robert, L.S., Singh, J.A.,
 Spott, B., and Tinker, N.A.
 A cDNA library prepared from Fusarium graminearum grown on a
 complex plant substrate
 Unpublished (2003)
 Contact: Watson, Robert J.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
 CANADA
 Tel: (613) 759-1655
 Fax: (613) 759-1701
 Email: watsonrj@agr.gc.ca

FEATURES
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 1..921
 Location/Qualifiers
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 /mol_type="mRNA"
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 /db_xref="taxon:5518"
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 /lab_host="E. coli DH10B"
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 /notes="Vector: pBluescript II+; Site_1: EcoRI; Site_2:
 XhoI; Fusarium graminearum grown on a complex plant
 substrate-- wheat leaves treated to remove most of the low
 molecular weight, water-soluble components."

Query Match 11.2%; Score 83.4; DB 6; Length 921;

Best Local Similarity 52.4%; Pred. No. 2.2e-12;
 Matches 208; Conservative 0; Mismatches 186; Indels 3; Gaps 1;
 QY 281 CCATAAAGTACGGAGCAACTTCCCAACCAATGTAATCGTATTTATGCTCTATGTT 340
 Db 363 CCATCAACTACGGAGGTTCTTCAACCTCAGGGTAACGGATACCTTTGCGTTTACGGAT 422
 QY 341 GGACTGTTGACCTCTGTTGGAATATATATGTCGACAGTTGGGGCACTGGCGTCCAC 400
 Db 423 GGACCCGGGTCCTCGTGGAGTACTACGTCGAGAGTTAGCGTTCTTACAAACCCG 482
 QY 401 CAGG---GCAACGCCCTTAAGGGACCACTACTGTTGATGGAGAACATATATCTACG 457
 Db 483 GCAGCCAGGCTCAGCACCGAGGTACCGTCTACACCGACGGTGACACCTTACGATCTCTATA 542
 QY 458 AGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTGCCACATTTAAACAATATGGA 517
 Db 543 TGTCCACCCGTTACACAGCGCTTCGATCGAGCGTTCAGACCTTCAACAGTACTGTT 602
 QY 518 GTGTTGGAAGATGGAACGACGAGTGGCAAGATTTCTGTGACGAACACATTTAGAGCGT 577
 Db 603 CCATCCGCGCAACAGCGTACCAGCGGCTCCGTCACATCGAGAACCACTTCAATGCTT 662
 QY 578 GGGAAACTTAGGGATGATATATGGGGAATGATGAAGTCGCTTACTGTAGAGGCT 637
 Db 663 GGAGATCTGCTGGCATGAACCTCGGAAACCACTTACTACGATTTCTGCCACTGAGGTT 722
 QY 638 ATCAAAGTAGCGAGTGTCTAATGTTATATAGCAATAC 674
 Db 723 ACCAGAGCAGTGGCTCATCTTCTATCTATGTCAGAC 759

RESULT 8
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 LOCUS mgxb0006C21r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 DEFINITION clone mgxb0006C21r, genomic survey sequence.
 AQ160513
 AQ160513.1 GI:3557502

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 1 (bases 1 to 603)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 Unpublished (1998)
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: GGAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 424.
 Location/Qualifiers

FEATURES
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 /organism="Magnaporthe grisea"
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 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice Blast BAC Library"
 /notes="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with

TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 JOURNAL Genome
 COMMENT Unpublished (1998)
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: GGAAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 321.

FEATURES

Location/Qualifiers
 1..720

/organism="Magnaporthe grisea"
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 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice Blast BAC Library"
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."

ORIGIN

Query Match 11.0%; Score 82.2; DB 8; Length 720;
 Best Local Similarity 54.1%; Pred. No. 4.5e-12;
 Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;
 QY 229 AAAGGTAAAAAATTCATGAAACACAAACACCAACCAAGTTGGTAACATGTCCATAAAC 288
 DB 445 AAAGGAAAAAAGAGACTTAACAAACAAACAAACAAAAA-----CAGCCGCGTCATCAAC 391
 QY 289 TAGGAGCCCACTTCACCAACCAATGTAATGCGTATTTATGCGTCTATGTTGGACTGTT 348
 DB 390 TACTCGGGCAGCTACAGCCNCAGGGCAACTCATACCTGGCCGCTCTACGGCTGGACGCGC 331
 QY 349 GACCCCTCTTGTGCAATATTATATTGTCGAGTTGGGCAACTGGCGTCCACCA---GGA 405
 DB 330 AACCCGCTGATCAGTACTACGTGGTGAGAGCTTTGGCAGCTACAAACCGCTGTCGGGC 271
 QY 406 GCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATATCTACGAGACTCTT 465
 DB 270 GCCACCAACCGCGGTCTTCACTCGGAGCGAGCCTACGACATCTGTTGTCAGCACC 211
 QY 466 AGAGTCAATCAACCTTCATTAAGGGATTGCGACATTTAAACAATATTGGAGTTGCA 525
 DB 210 CGCTACAACACGACCTTCATCGAGCGGCAACCAAGACCTTTTCAGCAGTTCTGTCGTCGCGC 151
 QY 526 AGATCGAAGACGACGAGTGGCAGATTCTGTCGAGCAACCATTTTATAGGCGTGGGAAAC 585
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 QY 586 TTAGGAGTGAATATGGGAAAAATGTATGAAGTCGCG---CTTACTGTAGAAGCTATCAA 642
 DB 90 GCGGGCTCAACTCGCACACAGTGAAGTACCAGATCTGCGCGCTCGAGGCTACCAC 31
 QY 643 AGTAGCGGAAGTGCTA 658
 DB 30 AGCAGCGGCTCCGCCA 15

RESULT 11

AQ160254/c
 LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: GGAAACAGCTATGACCATG

Class: BAC ends

High quality sequence stop: 344.

Location/Qualifiers

1..750

/organism="Magnaporthe grisea"

/mol_type="genomic DNA"

/strain="70-15"

/db_xref="taxon:148305"

/clone="mgxb0003L19r"

/tissue_type="Protoplasts"

/lab_host="E. coli DH10B"

/clone_lib="CUGI Rice Blast BAC Library"

/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."

ORIGIN

Query Match 11.0%; Score 82.2; DB 8; Length 750;
 Best Local Similarity 54.1%; Pred. No. 4.5e-12;
 Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;
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 QY 289 TAGGAGCCCACTTCACCAACCAATGTAATGCGTATTTATGCGTCTATGTTGGACTGTT 348
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 QY 406 GCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATATCTACGAGACTCTT 465
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 QY 466 AGAGTCAATCAACCTTCATTAAGGGATTGCGACATTTAAACAATATTGGAGTTGCA 525
 DB 210 CGCTACAACACGACCTTCATCGAGCGGCAACCAAGACCTTTTCAGCAGTTCTGTCGTCGCGC 151
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 QY 586 TTAGGAGTGAATATGGGAAAAATGTATGAAGTCGCG---CTTACTGTAGAAGCTATCAA 642
 DB 90 GCGGGCTCAACTCGCACACAGTGAAGTACCAGATCTGCGCGCTCGAGGCTACCAC 31
 QY 643 AGTAGCGGAAGTGCTA 658
 DB 30 AGCAGCGGCTCCGCCA 15

AQ160254
 mgxb0003L19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0003L19r, genomic survey sequence.

AQ160254
 AQ160254.1 GI:3557243

GSS.
 Magnaporthe grisea (anamorph: Pyricularia grisea)

Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 750)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome
 Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: GGAAACAGCTATGACCATG

Class: BAC ends

High quality sequence stop: 344.

Location/Qualifiers

1..750

/organism="Magnaporthe grisea"

/mol_type="genomic DNA"

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/clone="mgxb0003L19r"

/tissue_type="Protoplasts"

/lab_host="E. coli DH10B"

/clone_lib="CUGI Rice Blast BAC Library"

/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."

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Db 210 CGCTAACACAGCCCTCCATCGACGGCACCAAGACCTTTACAGATTCTGGTGGTGCGC 151
Qy 526 AGATCGAAACGACGAGTGGACAGTTCCTCTCAGCACCACTTTAGAGCGTGGAAAC 585
Db 150 CGCAACAAGCGCGGACGCGACCGTCACTTTGCCAACCAACGCTCAAGCGCTGGCGCAAC 91
Qy 586 TTAGGGATGAATATGGGAAAAATGTATGAAGTTCGCG---CTTACTGTAGAAGGCTATCAA 642
Db 90 GCGGCTCACTCGGCAACCAAGTGGAACTACCAAGATCCTGGCGTGGAGGCTACCAAC 31
Qy 643 AGTAGCGGAAGTGCTA 658
Db 30 AGCAGCGGCTCGCCA 15

RESULT 12
LOCUS AQ325248 786 bp DNA linear GSS 08-JAN-1999
DEFINITION mgxb0021M08r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0021M08r, genomic survey sequence.
ACCESSION AQ325248
VERSION AQ325248.1 GI:4117100
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 786)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 49
High quality sequence stop: 468.
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/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

FEATURES
source
Query Match 11.0%; Score 81.6; DB 8; Length 786;
Best Local Similarity 54.1%; Pred No. 6.8e-12;
Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;
Qy 229 AAAGTAAATAATTCATGAACACAAACACCAACCAAGTGGTGAACATGTCCATAAAC 288
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Qy 526 AGATCGAAACGCGAGTGGCAGATTTCTGTGACGCAACCACTTTAGAGCGTGGAAAC 585
Db 205 CGCAACAAGCGCGCACGCGGCGCCGTCACCTTTTGCCAAACCAACGCTCAACGCGCTG 146
Qy 586 TTAGGGATGAATATGGGAAAAATGTATGAAGTTCGCG---CTTACTGTAGAAGGCTATCAA 642
Db 145 GCGGCTCAACCTCGGCAACCAAGTGGAACTACCAAGATCCTGGCGCTCGAGGGCTACC 86
Qy 643 AGTAGCGGAAGTGCTA 658
Db 85 AGCAGCGGCTCGCCA 70

RESULT 13
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DEFINITION mgxb0001B24f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0001B24f, genomic survey sequence.
ACCESSION AQ399120
VERSION AQ399120.1 GI:4370147
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 583)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 411.
Location/Qualifiers
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/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
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containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

FEATURES
source
Query Match 11.0%; Score 81.6; DB 8; Length 786;
Best Local Similarity 54.1%; Pred No. 6.8e-12;
Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;
Qy 229 AAAGTAAATAATTCATGAACACAAACACCAACCAAGTGGTGAACATGTCCATAAAC 288
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```


COMMENT

Contact: Keon J
Plant Pathogen Interactions Division,
Rothamsted Research,
Harpenden, Herts, UNITED KINGDOM
Tel: +44(0)1582 763133
Fax: +44(0)1582 760981
Email: john.keon@bbsrc.ac.uk
Insert Length: 800 Std Error: 100.00
Seq primer: M13 reverse.
Location/Qualifiers
1..617
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/strain="Strit"
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/clone="mgcl2d03f"
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FEATURES

source

ORIGIN

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Best Local Similarity 55.6%; Pred. No. 1.9e-10;
Matches 168; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

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Db      |||||
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Db      |||||
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Db      |||||
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QY 485 AAACCAACCGGTGTCAACCAAGCCCTCCATTGACGCAACGAGACCTTTTCAGCAACTTCTGGA 544
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Db      ||
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Job time : 3227.17 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 15:57:32 ; Search time 7319.01 Seconds
(without alignments)
9775.823 Million cell updates/sec

Title: US-09-909-207-10
Perfect score: 1513
Sequence: 1 AAATTGAATTGGTATATCT.....TGAACACCTCGTCACTAG 1513

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1513	100.0	1513	6	A48232 Sequence 11
3	1513	100.0	1513	6	AR193055 Sequence
4	1513	100.0	1513	6	AR193056 Sequence
5	744	49.2	744	6	A48225 Sequence 4
6	744	49.2	744	6	A48226 Sequence 5
7	744	49.2	744	6	AR193051 Sequence
8	744	49.2	744	6	AR193052 Sequence
9	713.6	47.2	744	6	A68006 Sequence 1
10	713.6	47.2	744	6	AR163110 Sequence
11	673.6	44.5	744	6	A45313 Sequence 18
12	673.6	44.5	744	6	AR117325 Sequence
13	663	43.8	663	6	A48222 Sequence 1
14	663	43.8	663	6	A48223 Sequence 2
15	663	43.8	663	6	AR193049 Sequence
16	663	43.8	663	6	AR193050 Sequence
17	619	40.9	619	6	A48233 Sequence 12
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25	282.8	18.7	1022	6	A42285	Sequence 35
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39	274.4	18.1	684	1	AF220528	AF220528 Bacillus
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42	272.8	18.0	681	6	AR127045	AR127045 Sequence
43	272.8	18.0	681	6	AR127046	AR127046 Sequence
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ALIGNMENTS

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LOCUS	Sequence 10 from Patent EP0698667.					
DEFINITION	A48231					
ACCESSION	A48231					
VERSION	A48231.1	GI:2302078				
KEYWORDS	unidentified					
SOURCE	unidentified					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 1513)					
AUTHORS	De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.					
TITLE	Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof					
JOURNAL	Patent: EP 0698667-A 10 28-FEB-1996;					
COMMENT	SOLVAY (BE)					
	Other publication BE 1008751 960702					
	Other publication BE 1008570 960604					
	Other publication BR 9503454 960305					
	Other publication JP 8092284 960409					
	Other publication FI 953578 960127					
	Other publication CA 2154628 960127					
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Db 721 CATTTGCAACACGATGGCTATGATTAATGAAATTTTGGAAAGATAGCGGTGGCTCTGGAC 780
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Db 781 AATGATTTCTCAATCATGCGGTAGCTTCAATGAGTCCCAATGGAACAATGTTAAACAATTT 840
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Qy 1501 CCTCCGTCACCTAG 1513
Db 1501 CCTCCGTCACCTAG 1513
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RESULT 3
AR193055 1513 bp DNA linear PAT 20-APR-2002
LOCUS AR193055
DEFINITION Sequence 10 from patent US 6346407.
ACCESSION AR193055
VERSION AR193055.1 GI:20239020
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1513)
AUTHORS De Buy, E., Lahaye, A., Ledoux, P. and Detroz, R.
TITLE Xylanase, microorganisms producing it, DNA molecules, methods for
preparing this xylanase and uses of the latter
JOURNAL Patent: US 6346407-A 10 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..1513
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/mol_type="unassigned DNA"
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Query Match 100.0%; Score 1513; DB 6; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.5e-295;
Matches 1513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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 LOCUS 1513 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 11 from patent US 6346407.
 ACCESSION AR193056
 VERSION AR193056.1 GI:20239021
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1513)
 AUTHORS De Buy, E., Lahaye, A., Ledoux, P. and Detroz, R.
 TITLE Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
 JOURNAL Patent: US 6346407-A 11 12-FEB-2002;
 FEATURES
 source Location/Qualifiers
 1. 1513
 /organism="unknown"
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ORIGIN
 Query Match 100.0%; Score 1513; DB 6; Length 1513;
 Best Local Similarity 100.0%; Pred. No. 1.5e-295;
 Matches 1513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATGGAATGCTGATATCTTAATGATAACGCAAAATCGTCACTGTTTAACTAACTCTC 60
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Db 481 GATAATTATCCAGTTTCAAAATTTGAAATAGTGTGTATGAATAGTTTCAATGTCAACTG 540
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 Db 1441 TTTTATTGGAAGGTTAAGTATAGTATATCTCCGATTCATCCAGAGAAATGCTTTGAAACA 1500
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RESULT 5
A48225

LOCUS A48225 744 bp DNA linear PAT 07-MAR-1997
 DEFINITION Sequence 4 from Patent EP0698667.
 ACCESSION A48225
 VERSION A48225.1 GI:2302072
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified
 1 (bases 1 to 744)
 De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
 Xylanase, microorganisms for its production, DNA molecules, process
 of preparation and use thereof
 Patent: EP 0698667-A 4 28-FEB-1996;
 SOLVAY (BE)
 COMMENT Other publication BE 1008751 960702
 Other publication BE 1008570 960604
 Other publication BR 9503454 960305
 Other publication JP 8092284 960409
 Other publication FI 953578 960127
 Other publication CA 2154628 960127
 Other publication AU 2508695 960208.
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 Query Match 49.2%; Score 744; DB 6; Length 744;
 Best Local Similarity 100.0%; Pred. No. 3.9e-140;
 Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 620 ATGAGCAAAAGAAATTCAGCTGTTGATTTTAGCTTTTGTAGTTTGTTCGACTTAACCTTA 679
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Qy      1340  AGCATAACTTTGGATAAAACAAT 1363
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RESULT 6
LOCUS      A48226          744 bp      DNA      linear      PAT 07-MAR-1997
DEFINITION Sequence 5 from Patent EP0698667.
ACCESSION A48226
VERSION   A48226.1  GI:2302073
KEYWORDS  .
SOURCE    unidentified
           unidentified
           unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS   De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE      Xylanase, microorganisms for its production, DNA molecules, process
           of preparation and use thereof
JOURNAL    Patent: EP 0698667-A 5 28-FEB-1996;
           SOLVAY (BE)
COMMENT    Other publication BE 1008751 960702
           Other publication BE 1008570 960604
           Other publication JP 9503454 960305
           Other publication JP 8092284 960409
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Query Match      49.2%; Score 744; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.9e-140;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      620  ATGAGACAAAAGAAATGACGTTGATTTTAGCCCTTTTAGTTGTTTGGCACTAACCTTA 679
Db      1  ATGAGACAAAAGAAATGACGTTGATTTTAGCCCTTTTAGTTGTTTGGCACTAACCTTA 60
Qy      680  CCTGAGAAATTAATTCAGGCAAAATCGTCACCGCAATTCATTCGGCAACACGATGCG 739
Db      61  CCTGAGAAATTAATTCAGGCAAAATCGTCACCGCAATTCATTCGGCAACACGATGCG 120
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Db      181  GGTACGTTACGTCGCCCAATGGAACAATGTTTAAACAATATTATTCCGTAAGGTTAAAAA 240
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Db      241  TTCAATGAAACACAAAACACACAACTGTTGTAACATGTCCATAAACTACGGAGCCCAAC 300
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Db      301  TTCCAACCAAAATGGTAAATGCGTATTATTATGCGTCTATGTTGGACTGTTTGACCCCTCTTGT 360
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Qy      1340  AGCATAACTTTGGATAAAACAAT 1363
Db      721  AGCATAACTTTGGATAAAACAAT 744

RESULT 7
LOCUS      AR193051          744 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6346407.
ACCESSION AR193051
VERSION   AR193051.1  GI:20239016
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 744)
AUTHORS   De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R.
TITLE      Xylanase, microorganisms producing it, DNA molecules, methods for
           preparing this xylanase and uses of the latter
JOURNAL    Patent: US 6346407-A 4 12-FEB-2002;
           Location/Qualifiers
FEATURES             source
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Query Match      49.2%; Score 744; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.9e-140;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 GGTAGCTTCAGTCCCAATGGAACAAATGTTTAAACAATATTTCCGTAAGGTAAAAA 240

Qy 860 TTTCAATGAACAAACAAACAAACAAAGTTGGTAAACATGTCATATAAATACGAGCCAAAC 919

Db 241 TTTCAATGAACAAACAAACAAACAAAGTTGGTAAACATGTCATATAAATACGAGCCAAAC 300

Qy 920 TTTCCAAACCAATGTTAAATGCGTATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTG 979

Db 301 TTTCCAAACCAATGTTAAATGCGTATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTG 360

Qy 980 GAATATTATTTGTCGACAGTTGGGCAACTGCGCTCCACAGGAGCAACGGCTTAAGGGG 1039

Db 361 GAATATTATTTGTCGACAGTTGGGCAACTGCGCTCCACAGGAGCAACGGCTTAAGGGG 420

Qy 1040 ACCATCACTGTTGATGGAGCAATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 1099

Db 421 ACCATCACTGTTGATGGAGCAATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480

Qy 1100 TCCATTAAAGGGGATTCGCCACATTTAAACAATATTGGAGTGTTCGAAAGATCGAAACGCACG 1159

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Qy 1340 AGCATAACTTTGGATAAAAAACAAT 1363

Db 721 AGCATAACTTTGGATAAAAAACAAT 744

RESULT 8

LOCUS AR193052 744 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 5 from patent US 6346407.

ACCESSION AR193052

VERSION AR193052.1 GI:20239017

KEYWORDS Unknown.

SOURCE Unclassified.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 744)

AUTHORS De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.

TITLE Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter

JOURNAL Patent: US 6346407-A 5 12-FEB-2002;

FEATURES

source Location/Qualifiers

1..744

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 49.2%; Score 744; DB 6; Length 744;

Best Local Similarity 100.0%; Pred. No. 3.9e-140;

Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 ATGACAAAGAAATGACGTTGATTTAGCCCTTTTGTGTTGTTGCACTAACCTTA 679

Db 1 ATGACAAAGAAATGACGTTGATTTAGCCCTTTTGTGTTGTTGCACTAACCTTA 60

Qy 680 CTTGAGAAATTAATTCAGGCAAAATCGTCAACGCAAAATTCATTGGCAACCCACGATGCG 739

Db 61 CTTGAGAAATTAATTCAGGCAAAATCGTCAACGCAAAATTCATTGGCAACCCACGATGCG 120

Qy 740 TATGATTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCTCAATCATGCG 799

Db 121 TATGATTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCTCAATCATGCG 180

Qy 800 GGTAGCTTCAGTCCCAATGGAACAAATGTTTAAACAATATTTCCGTAAGGTAAAAA 859

Db 181 GGTAGCTTCAGTCCCAATGGAACAAATGTTTAAACAATATTTCCGTAAGGTAAAAA 240

Qy 860 TTTCAATGAACAAACAAACAAACAAAGTTGGTAAACATGTCATATAAATACGAGCCAAAC 919

Db 241 TTTCAATGAACAAACAAACAAACAAAGTTGGTAAACATGTCATATAAATACGAGCCAAAC 300

Qy 920 TTTCCAAACCAATGTTAAATGCGTATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTG 979

Db 301 TTTCCAAACCAATGTTAAATGCGTATTTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTG 360

Qy 980 GAATATTATTTGTCGACAGTTGGGCAACTGCGCTCCACAGGAGCAACGGCTTAAGGGG 1039

Db 361 GAATATTATTTGTCGACAGTTGGGCAACTGCGCTCCACAGGAGCAACGGCTTAAGGGG 420

Qy 1040 ACCATCACTGTTGATGGAGCAATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 1099

Db 421 ACCATCACTGTTGATGGAGCAATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480

Qy 1100 TCCATTAAAGGGGATTCGCCACATTTAAACAATATTGGAGTGTTCGAAAGATCGAAACGCACG 1159

Db 481 TCCATTAAAGGGGATTCGCCACATTTAAACAATATTGGAGTGTTCGAAAGATCGAAACGCACG 540

Qy 1160 AGTGCCACGATTTCTGTGACCAACCACTTTAGAGCGTGGAAAACTTAGGGATGAATATG 1219

Db 541 AGTGCCACGATTTCTGTGACCAACCACTTTAGAGCGTGGAAAACTTAGGGATGAATATG 600

Qy 1220 GGGAAAATGATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAGTGCCTAAT 1279

Db 601 GGGAAAATGATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAGTGCCTAAT 660

Qy 1280 GTATATAGCAATACACTAAGAAATTAACGGTAAACCCCTCTCAACTATTAGTATGACGAG 1339

Db 661 GTATATAGCAATACACTAAGAAATTAACGGTAAACCCCTCTCAACTATTAGTATGACGAG 720

Qy 1340 AGCATAACTTTGGATAAAAAACAAT 1363

Db 721 AGCATAACTTTGGATAAAAAACAAT 744

RESULT 9

LOCUS A68006 744 bp DNA linear PAT 05-MAY-1999

DEFINITION Sequence 1 from Patent WO9743409.

ACCESSION A68006

VERSION A68006.1 GI:4756810

KEYWORDS unidentified

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 744)

AUTHORS Dalboe, H., Diderichsen, B., Sandal, T. and Kauppinen, S.

TITLE METHOD OF PROVIDING NOVEL DNA SEQUENCES

JOURNAL Patent: WO 9743409-A 1 20-NOV-1997;

NOVONORDISK AS (DK)

FEATURES

source Location/Qualifiers

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/notes="unnamed protein product"

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CDS


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A45313
LOCUS       A45313               744 bp      DNA      linear      PAT 07-MAR-1997
DEFINITION  Sequence 18 from Patent WO9518219.
ACCESSION   A45313
VERSION     A45313.1  GI:2299796
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 744)
AUTHORS     Van,S.P., Williams,D.P., Iverson,S., Farrell,R.L., Herbes,W.T.,
            Van,D.K., Herweijer,M.A., Van,B.R., Quax,W.J., Goedegebuur,F. and
            Jones,B.E.
TITLE       ALKALI-TOLERANT XYLANASES
JOURNAL     Patent: WO 9518219-A 18 06-JUL-1995;
COMMENT     GIST BROCADES NV (NL)
            Other publication JP 8507221T 960806
            Other publication BR 9405934 951226
            Other publication NO 953312 951019
            Other publication FI 953920 950821
            Other publication AU 1415095 950717.

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ORIGIN
Query Match      44.5%; Score 673.6; DB 6; Length 744;
Best Local Similarity 95.7%; Pred. No. 6.5e-126;
Matches 714; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

QY      620  ATGAGCAAAAGAAATTGACGTTGATTTAGCCCTTTTGTAGCTTTTGTGACCTAACTTA 679
DB      1   ATGAGCCAAAGAAATTGACGTTGA--TTAACCTTTTGTAGTTTG-TTTGCACTAACTTA 57

QY      680  CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCATTTGGCAACACGATGCC 739
DB      58  CCTGCAAGAATAAGTCAGGCACAAATCGTCACCGACAATTCATTTGGCAACACGATGCC 117

QY      740  TATGATTATCAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGC 799
DB      118  TATGATTATCAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGC 177

QY      800  GGTAAGTTCAAGTCCCAATGGAAACAATGTTTAAACAATATTTATTCGTAAGGTAAGAAA 859
DB      178  GGTAAGTTCAAGTCCCAATGGAAACAATGTTTAAACAATATTTATTCGTAAGGTAAGAAA 237

QY      860  TTCATGAAACAAACACACACCAAGTGGTAACATGTCATTAACACGAGGCAAC 919
DB      238  TTCATGAAACAAACACACCAAGTGGTAACATGTCATTAACACGAGGCAAC 297

QY      920  TTCAACCAATATGATGCGTATTTATGCGTCTATGCTTGGACTGTGACCCCTCTTGTC 979
DB      298  TTCAACCAATATGATGCGTATTTATGCGTCTATGCTTGGACTGTGACCCCTCTTGTC 357

QY      980  GAATATTATATGTCGACAGTTGGGCAACTGGCGTCCACAGAGCAACGCTTAAGGG 1039
DB      358  GAATATTATATGTCGACAGTTGGGCAACTGGCGTCCACAGAGCAACGCTTAAGGG 417

QY      1040 ACCATCACTGTTGATGGAGNACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 1099
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QY      1100  TCCATTAAAGGGATTGCCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG 1159
DB      478  TCCATTAAAGGGATTGCCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG 537
QY      1160  AGTGGCAGGATTTCTGTCTAGCAACCACTTTTAGAGCGTGGGAAACTTAGGGATGAATATG 1219
DB      538  AGTGCCACAATTTCTGTCTAGCAACCACTTTTAGAGCGTGGGAAACTTAGGGATGAATATG 597
QY      1220  GGGAAATGTTATGAAGTCGCGCTTACTCTAGAGGCTATCAAGTAGCGGAAGTCTTAT 1279
DB      598  GGGAAATGTTATGAAGTCGCGCTTACTCTAGAGGCTATCAAGTAGCGGAAGTCTTAT 657
QY      1280  GTATATACCAATACACTAAGAAATTAACGTAACCCCTCTCAACTATTAGTAAATGACGAG 1339
DB      658  GTATATACCAATACACTAAGAAATTAACGTAACCCCTCTCAACTATTAGTAAATGACGAG 717
QY      1340  AGCATAACTTTGGATAAAAAACAATTA 1365
DB      718  AGCATAACTCTAGATAAAAAACAATTA 743

RESULT 12
LOCUS     AR117325               744 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION  Sequence 18 from patent US 6140095.
ACCESSION   AR117325
VERSION     AR117325.1  GI:14098231
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 744)
AUTHORS     Williams,D.P., Iverson,S., Farrell,R.Lee., Van Solingen,P.,
            Herbes,W.Theresia., Van Der Kleij,W.Antonius.H., Van
            Beckhoven,R.Francisus.C., Quax,W.Johannes., Herwijer,M.Adriana.,
            Goedegebuur,F. and Jones,B.Edward.
TITLE       Alkalitolerant xylanases
JOURNAL     Patent: US 6140095-A 18 31-OCT-2000;
FEATURES             Location/Qualifiers
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ORIGIN
Query Match      44.5%; Score 673.6; DB 6; Length 744;
Best Local Similarity 95.7%; Pred. No. 6.5e-126;
Matches 714; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

QY      620  ATGAGCAAAAGAAATTGACGTTGATTTAGCCCTTTTGTAGCTTTTGTGACCTAACTTA 679
DB      1   ATGAGCCAAAGAAATTGACGTTGA--TTAACCTTTTGTAGTTTG-TTTGCACTAACTTA 57

QY      680  CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCATTTGGCAACACGATGCC 739
DB      58  CCTGCAAGAATAAGTCAGGCACAAATCGTCACCGACAATTCATTTGGCAACACGATGCC 117

QY      740  TATGATTATCAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGC 799
DB      118  TATGATTATCAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGC 177

QY      800  GGTAAGTTCAAGTCCCAATGGAAACAATGTTTAAACAATATTTATTCGTAAGGTAAGAAA 859
DB      178  GGTAAGTTCAAGTCCCAATGGAAACAATGTTTAAACAATATTTATTCGTAAGGTAAGAAA 237

QY      860  TTCATGAAACAAACACACCAAGTGGTAACATGTCATTAACACGAGGCAAC 919
DB      238  TTCATGAAACAAACACCAAGTGGTAACATGTCATTAACACGAGGCAAC 297

QY      920  TTCAACCAATATGATGCGTATTTATGCGTCTATGCTTGGACTGTGACCCCTCTTGTC 979
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 Db 358 GAATATTATTTGTCGACAGTTGGGCACTGGCGTCCACAGGAGCAACGCTTAAGGGA 417
 QY 1040 ACCATCACTGTTGATGGAGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCC 1099
 Db 418 ACCATCACTGTTGATGGAGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCC 477
 QY 1100 TCATTAAGGGATTGCCACATTTAAACATATTTGGAGTTCGAAGATCGAAACGACG 1159
 Db 478 TCCATTAAGGGATTGCCACATTTAAACATATTTGGAGTTCGAAGATCGAAACGACG 537
 QY 1160 AGTGGCAGCATTTCTGTGACGCAACCACTTTAGAGCGTGGGAACTTTAGGAGTGAATG 1219
 Db 538 AGTGGCAGCATTTCTGTGACGCAACCACTTTAGAGCGTGGGAACTTTAGGAGTGAATG 597
 QY 1220 GGGAAATGATGAAGTGCCTTACTGTAGAGGCTATCAAGTAGCGGAGTCTTAAT 1279
 Db 598 GGGAAATGATGAAGTGCCTTACTGTAGAGGCTATCAAGTAGCGGAGTCTTAAT 657
 QY 1280 GTATATAGCAATACACTAAGATTAACCGTAAACCTCTCTCACTATTAGTAATGACGAG 1339
 Db 658 GTATATAGCAATACACTAAGATTAACCGTAAACCTCTCTCACTATTAGTAATGACGAG 717
 QY 1340 AGCATAACTTTGGATAAAAAACAATTA 1365
 Db 718 AGCATAACTCTAGATAAAAAACAATTA 743

RESULT 13
 A48222
 LOCUS A48222 663 bp DNA linear PAT 07-MAR-1997
 DEFINITION Sequence 1 from Patent EP0698667.
 ACCESSION A48222
 VERSION A48222.1 GI:2302069
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified

REFERENCE 1 (bases 1 to 663)
 De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
 Xylanase, microorganisms for its production, DNA molecules, process
 of preparation and use thereof
 Patent: EP 0698667-A 1 28-FEB-1996;
 JOURNAL SOLVAY (BE)
 COMMENT Other publication BE 1008751 960702
 Other publication BE 1008570 960604
 Other publication BR 9503454 960305
 Other publication JP 8092284 960409
 Other publication FI 953578 960127
 Other publication CA 2154628 960127
 Other publication AU 2508695 960208.

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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 9.1e-124;
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 CAAATCGTCACCGACAATTCATTTGGCAACCAACGATGCTATGATTATGATTTGGAA 760
 Db 1 CAAATCGTCACCGACAATTCATTTGGCAACCAACGATGCTATGATTATGATTTGGAA 60
 QY 761 GATACGGTGGCTCTGGGACAAATGTTCTCAATCATGCGGTAGCTTCAGTGGCCCAATGG 820
 Db 61 GATACGGTGGCTCTGGGACAAATGTTCTCAATCATGCGGTAGCTTCAGTGGCCCAATGG 120

QY 821 AACCAATGTTAAACAATATTTATTCGTAAGAGTAAAAAATTCATATGAACACAAACACAC 880
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 QY 881 CAAACAAGTTGGTAACTGTCATATAAATCTACGAGCCAACTTTCCAAACCAATATGGTAATGCG 940
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 Db 241 TATTATGCGTCTATGTTGGAGTGTGACCTCTTCTCGAATATTTATTTGTCGACAGT 300
 QY 1001 TGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCACTCTGTTGATGGAGGA 1060
 Db 301 TGGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCACTCTGTTGATGGAGGA 360
 QY 1061 ACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCTCCATTAAGGGGATTTGCCACA 1120
 Db 361 ACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCTCCATTAAGGGGATTTGCCACA 420
 QY 1121 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTCTCAGC 1180
 Db 421 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGATTTCTGTCTCAGC 480
 QY 1181 AACCACTTTTAGAGCGTGGGAAACTTTAGGAGTGAATATGCGGAAATATGTAAGAGTGGCG 1240
 Db 481 AACCACTTTTAGAGCGTGGGAAACTTTAGGAGTGAATATGCGGAAATATGTAAGAGTGGCG 540
 QY 1241 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAATGTATATAGCAATACACTAAGA 1300
 Db 541 CTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTAATGTATATAGCAATACACTAAGA 600
 QY 1301 ATTAACGCTAACCTCTCTCAACTATTAGTAATGACGAGAGCATAAATTTGGATAAAAAAC 1360
 Db 601 ATTAACGCTAACCTCTCTCAACTATTAGTAATGACGAGAGCATAAATTTGGATAAAAAAC 660
 QY 1361 AAT 1363
 Db 661 AAT 663

RESULT 14
 A48223
 LOCUS A48223 663 bp DNA linear PAT 07-MAR-1997
 DEFINITION Sequence 2 from Patent EP0698667.
 ACCESSION A48223
 VERSION A48223.1 GI:2302070
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified

REFERENCE 1 (bases 1 to 663)
 De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
 Xylanase, microorganisms for its production, DNA molecules, process
 of preparation and use thereof
 Patent: EP 0698667-A 2 28-FEB-1996;
 JOURNAL SOLVAY (BE)
 COMMENT Other publication BE 1008751 960702
 Other publication BE 1008570 960604
 Other publication BR 9503454 960305
 Other publication JP 8092284 960409
 Other publication FI 953578 960127
 Other publication CA 2154628 960127
 Other publication AU 2508695 960208.

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ORIGIN		Query Match	43.8%; Score 663; DB 6; Length 663;	
		Best Local Similarity	100.0%; Pred. No. 9.1e-124;	
		Matches 663; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	701	CAAAATCGTCACCGACAAATTCATTTGGCAACACGATGGCTATGATTAATAATTTTGGAAA	760	
Db	1	CAAAATCGTCACCGACAAATTCATTTGGCAACACGATGGCTATGATTAATAATTTTGGAAA	60	
QY	761	GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGCTACGTTCAAGTCCCAATGG	820	
Db	61	GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGCTACGTTCAAGTCCCAATGG	120	
QY	821	AACAATGTTAAACAACATATTTATTCGTTAAAGGTAAATAATTCATGAAACACAAACACAC	880	
Db	121	AACAATGTTAAACAACATATTTATTCGTTAAAGGTAAATAATTCATGAAACACAAACACAC	180	
QY	881	CAACAAGTTGGTAACATGTCCTAAATACTACGAGGCCAATTCACCAACAAATGGTAATGG	940	
Db	181	CAACAAGTTGGTAACATGTCCTAAATACTACGAGGCCAATTCACCAACAAATGGTAATGG	240	
QY	941	TATTTATGCGTCTATGGTGGACTGTGACCTCTTGTGCAATATTAATTTGCGACAGT	1000	
Db	241	TATTTATGCGTCTATGGTGGACTGTGACCTCTTGTGCAATATTAATTTGCGACAGT	300	
QY	1001	TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGACCACTCACTGTTGATGGAGGA	1060	
Db	301	TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGACCACTCACTGTTGATGGAGGA	360	
QY	1061	ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGGCCACA	1120	
Db	361	ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGGCCACA	420	
QY	1121	TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGGATTTCTGTCAGC	1180	
Db	421	TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGGATTTCTGTCAGC	480	
QY	1181	AACCACTTTAGAGCGTGGGAAAACCTTAGGATGATATATGGGAAAATGTATGAAGTCGCG	1240	
Db	481	AACCACTTTAGAGCGTGGGAAAACCTTAGGATGATATATGGGAAAATGTATGAAGTCGCG	540	
QY	1241	CTTACTGTAGAAGCTATCAAGTAGCGGAAGTCTAATGATATATAGCAATACACTAAGA	1300	
Db	541	CTTACTGTAGAAGCTATCAAGTAGCGGAAGTCTAATGATATATAGCAATACACTAAGA	600	
QY	1301	ATTAAACGGTAACCTCTCTCAACTATTAGTAAAGCAGAGCATTAATTTGGATAAAAC	1360	
Db	601	ATTAAACGGTAACCTCTCTCAACTATTAGTAAAGCAGAGCATTAATTTGGATAAAAC	660	
QY	1361	AAT 1363		
Db	661	AAT 663		

RESULT 15
AR193049 LOCUS AR193049 563 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6346407.
ACCESSION AR193049
VERSION AR193049.1 GI:20239014
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 663)
De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for
preparing this xylanase and uses of the latter
Patent: US 6346407-A 1 12-FEB-2002;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN		Query Match	43.8%; Score 663; DB 6; Length 663;	
		Best Local Similarity	100.0%; Pred. No. 9.1e-124;	
		Matches 663; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	701	CAAAATCGTCACCGACAAATTCATTTGGCAACACGATGGCTATGATTAATAATTTTGGAAA	760	
Db	1	CAAAATCGTCACCGACAAATTCATTTGGCAACACGATGGCTATGATTAATAATTTTGGAAA	60	
QY	761	GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGCTACGTTCAAGTCCCAATGG	820	
Db	61	GATAGCGGTGGCTCTGGGCAATGATTTCTCAATCATGCGGCTACGTTCAAGTCCCAATGG	120	
QY	821	AACAATGTTAAACAACATATTTATTCGTTAAAGGTAAATAATTCATGAAACACAAACACAC	880	
Db	121	AACAATGTTAAACAACATATTTATTCGTTAAAGGTAAATAATTCATGAAACACAAACACAC	180	
QY	881	CAACAAGTTGGTAACATGTCCTAAATACTACGAGGCCAATTCACCAACAAATGGTAATGG	940	
Db	181	CAACAAGTTGGTAACATGTCCTAAATACTACGAGGCCAATTCACCAACAAATGGTAATGG	240	
QY	941	TATTTATGCGTCTATGGTGGACTGTGACCTCTTGTGCAATATTAATTTGCGACAGT	1000	
Db	241	TATTTATGCGTCTATGGTGGACTGTGACCTCTTGTGCAATATTAATTTGCGACAGT	300	
QY	1001	TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGACCACTCACTGTTGATGGAGGA	1060	
Db	301	TGGGGCAACTGGCGTCCACGAGGCAACGCTTAAGGGACCACTCACTGTTGATGGAGGA	360	
QY	1061	ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGGCCACA	1120	
Db	361	ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATGGCCACA	420	
QY	1121	TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGGATTTCTGTCAGC	1180	
Db	421	TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGGATTTCTGTCAGC	480	
QY	1181	AACCACTTTAGAGCGTGGGAAAACCTTAGGATGATATATGGGAAAATGTATGAAGTCGCG	1240	
Db	481	AACCACTTTAGAGCGTGGGAAAACCTTAGGATGATATATGGGAAAATGTATGAAGTCGCG	540	
QY	1241	CTTACTGTAGAAGCTATCAAGTAGCGGAAGTCTAATGATATATAGCAATACACTAAGA	1300	
Db	541	CTTACTGTAGAAGCTATCAAGTAGCGGAAGTCTAATGATATATAGCAATACACTAAGA	600	
QY	1301	ATTAAACGGTAACCTCTCTCAACTATTAGTAAAGCAGAGCATTAATTTGGATAAAAC	1360	
Db	601	ATTAAACGGTAACCTCTCTCAACTATTAGTAAAGCAGAGCATTAATTTGGATAAAAC	660	
QY	1361	AAT 1363		
Db	661	AAT 663		

Search completed: November 10, 2004, 21:26:31
Job time : 7322.01 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 10, 2004, 15:55:17 ; Search time 959.753 Seconds
(without alignments)
8275.436 Million cell updates/sec

Title: US-09-909-207-10
Perfect score: 1513
Sequence: 1 AATATTGAATTGGTATATCT.....TGAAACACCTCGTCACTAG 1513

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 23Sep04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1513	100.0	1513	2	AAT16103
2	840.6	55.6	871	2	AAT16103 Xylanase
3	744	49.2	744	2	AAT16102
4	713.6	47.2	744	2	AAT16102 Xylanase
5	673.6	44.5	744	2	AAT16102 Glycosyl
6	663	43.8	663	2	AAT16101
7	590.2	39.0	747	2	AAT16101 Xylanase
8	393	26.0	1068	12	AAT13074 Xylanase
9	282.8	18.7	1022	2	Adj34947 DNA encod
10	276.6	18.3	1956	12	AAT09023 B. pumilu
11	274.4	18.1	684	12	Adj35051 DNA encod
12	255.6	16.9	2364	3	Adj34969 DNA encod
13	217.2	14.4	1190	2	Aaz51821 Clostridi
14	204.8	13.5	1244	2	Aat90972 Nucleotid
15	177.8	11.8	747	12	Aat08142 Xylanase
16	154.4	10.2	164	2	Adj35011 DNA encod
17	151.2	10.0	164	2	Aat92876 Thermosta
18	143.6	9.5	1695	12	Aat92875 Thermosta
19	142.6	9.4	1338	12	Adj35101 DNA encod
20	136.2	9.0	1077	12	Adj35151 DNA encod
21	130.2	8.6	1065	12	Adj34965 DNA encod
					Adj34999 DNA encod

22	128.4	8.5	1047	12	ADJ34949	Adj34949 DNA encod
23	121.2	8.0	678	12	ADJ34955	Adj34955 DNA encod
24	119.4	7.9	1375	2	AAX90405	Aax90405 Actinomad
25	119.4	7.9	1375	2	AAT64930	Aat64930 Actinomad
26	119	7.9	229	2	AAV15063	Aav15063 Xylanase
27	118.4	7.8	573	2	AAV36098	Aav36098 DNA seque
28	117.8	7.8	1207	2	AAT42374	Aat42374 Bacillus
29	117.6	7.8	1041	12	ADJ34943	Adj34943 DNA encod
30	116.8	7.7	1047	12	ADJ35083	Adj35083 DNA encod
31	115.2	7.6	213	2	AAV15059	Aav15059 Xylanase
32	115.2	7.6	596	3	AAA48219	Aaa48219 T. reesei
33	115.2	7.6	596	6	ADJ29410	Adj29410 Trichoder
34	115.2	7.6	596	9	AAI60925	Aai60925 Trichoder
35	115.2	7.6	596	9	AAI60941	Aai60941 Trichoder
36	112	7.4	1074	12	ADJ34983	Adj34983 DNA encod
37	112	7.4	1137	12	ADJ35039	Adj35039 DNA encod
38	111.8	7.4	1273	2	AQ90388	Aaq90388 Xylanase
39	111.4	7.4	636	12	ADJ34981	Adj34981 DNA encod
40	111.4	7.4	942	10	ABQ80366	Abq80366 A. fumiga
41	111.2	7.3	1008	12	ADJ35015	Adj35015 DNA encod
42	110.8	7.3	669	12	ADJ34951	Adj34951 DNA encod
43	110.4	7.3	1047	12	ADJ35037	Adj35037 DNA encod
44	110	7.3	1002	10	ABQ80365	Abq80365 A. fumiga
45	109.4	7.2	1041	12	ADJ34953	Adj34953 DNA encod

ALIGNMENTS

RESULT 1
AAT16103
ID AAT16103 standard; DNA; 1513 BP.
XX AC AAT16103;
XX 16-OCT-2003 (revised).
DT 15-MAY-1996 (first entry)
XX Xylanase gene.
XX Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
KW ss.
XX Bacillus sp; strain 710/1 (LMG P-14798).
XX Key Location/Qualifiers
FH promoter 1..619
FT CDS /*tag= a
FT CDS 620..1366
FT sig_peptide /*tag= b
FT mat_peptide 620..600
FT /*tag= c
FT 701..1363
FT /*tag= d
FT /*tag= e
FT 1367..1513
FT 3'UTR /*tag= e
XX AU9525086-A.
XX 08-FEB-1996.
XX 19-JUL-1995; 95AU-00025086.
XX 26-JUL-1994; 94BB-00000706.
XX 17-MAY-1995; 95BB-00000448.
XX (SOLV) SOLVAY SA.
XX De Buyl E, Lahaye A, Ledoux P, Detroz R;
XX WPI; 1996-117341/13.
XX P-PSDB; AAR92054.

XX Bacillus derived xylanase active over wide pH range - used in treatment
PT of paper pulp, animal feeds and in bakery goods.
XX Claim 10; Page 59-61; 94pp; English.
XX A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was
CC isolated from a gene library of *Bacillus* sp. 720/1 (LMG P-14798). The
CC gene may be incorporated into a vector and expressed in transformed
CC hosts, pref. *Bacillus licheniformis* or *Bacillus pumilus*, for prodn. of
CC thermostable mature xylanase (AAR92053). The enzyme is useful in the
CC paper pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX Sequence 1513 BP; 500 A; 282 C; 271 G; 460 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1513; DB 2; Length 1513;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 A A A T T G A A T T G T G T A T A T C T A A T G A T A A G C A A A T C G T C A C T G T T T T A A C T A A T C T C 60
DB 1. A A A T T G A A T T G T G T A T A T C T A A T G A T A A G C A A A T C G T C A C T G T T T T A A C T A A T C T C 60
QY 61 A A A C C A A T A C T T C T T T A T T A A C G C T A A C C A C T T C T A A T C T T A T C A A G A A C A C A T T C T T T 120
DB 61' A A A C C A A T A C T T C T T T A T T A A C G C T A A C C A C T T C T A A T C T T A T C A A G A A C A C A T T C T T T 120
QY 121 A P A G A A C T T C C C A T T T G C A A G A C G A T A A A A A T C T T T T C C C C T A T T T A T C T T A T C G 180
DB 121 A P A G A A C T T C C C A T T T G C A A G A C G A T A A A A A T C T T T T C C C C T A T T T A T C T T A T C G 180
QY 181 C C T T G A T C G T T A A T T T G T A A C T T A T T T A G T T A G C T G A T G T T C C C T A T T C A T C A T A C 240
DB 181 C C T T G A T C G T T A A T T T G T A A C T T A T T T A G T T A G C T G A T G T T C C C T A T T C A T T C A T A C 240
QY 241 C A T T A A T C A C A G T T A A C G T C A G A T C A T C T T T T T C G G T T C T C A A A A T A C C T G A A G A A C 300
DB 241 C A T T A A T C A C A G T T A A C G T C A G A T C A T C T T T T T C G G T T C T C A A A A T A C C T G A A G A A C 300
QY 301 A T T T A T G T C A T A T T T C T C A C G C C G C T C A T A A T G A A T A T A T A T A C T T T T T A T A C A T A 360
DB 301 A T T T A T G T C A T A T T T C T C A C G C C G C T C A T A A T G A A T A T A T A T A C T T T T T A T A C A T A 360
QY 361 T T A A G T A A T T A G T A T A C T T G C G T T A C A A A A T G C A G A T A A T C T A A T T G A T C A A A C A 420
DB 361 T T A A G T A A T T A G T A T A C T T G C G T T A C A A A A T G C A G A T A A T C T A A T T G A T C A A A C A 420
QY 421 A G C A G T A T C C A A A A A C A C T G A T G T G A C C T T T A A A G A A G T G C A C T A T C T A T G A A A A 480
DB 421 A G C A G T A T C C A A A A A C A C T G A T G T G A C C T T T A A A G A A G T G C A C T A T C T A T G A A A A 480
QY 481 G A T A A T T A C C A G T T C A A A A T T G A A A T A G T G T G A T G G A A T A G T T G A A T G T C A A C T G 540
DB 481 G A T A A T T A C C A G T T C A A A A T T G A A A T A G T G T G A T G G A A T A G T T G A A T G T C A A C T G 540
QY 541 C T G T G A A G G A G G T A G T A G T A C C G T A G A C T T C A T T A C C A A A A A T T A G T T G T A A A A A A 600
DB 541 C T G T G A A G G A G G T A G T A G T A C C G T A G A C T T C A T T A C C A A A A A T T A G T T G T A A A A A A 600
QY 601 T T A A A G A G A A A T G C T A A T C A G A C A A A A A A T T G A C G T T G A T T T A G C C T T T T A G T 660
DB 601 T T A A A G A G A A T G C T A A T C A G A C A A A A A A T T G A C G T T G A T T T A G C C T T T T A G T 660
QY 661 T T G T T T T G C A C T T A C C T G C A G A A T A A T T C A G G C A C A A A T C G T C A C C G A C A A T T C 720
DB 661 T T G T T T T G C A C T T A C C T G C A G A A T A A T T C A G G C A C A A A T C G T C A C C G A C A A T T C 720
QY 721 C A T T G C C A C C A G T A G T A T A T A T A A T T T T G A A G A T A C G G T G G C T C T G G A C 780
DB 721 C A T T G C C A C C A G T A G T A T A T A T A A T T T T G A A G A T A C G G T G G C T C T G G A C 780
QY 781 A A T G A T T C T C A T C A T G C G G T A C G T T C A G T C C C A A T G G A A C A A T T T A C A C A T A T T 840

DB 781 A A T G A T T C T C A T C A T G C G G T A C G T T C A G T C C C A A T G G A A C A A T T T A C A C A T A T T 840
QY 841 A T T C C G T A A A G G T A A A A A T T C A A T G A A A C A A A C A C A C A A G T T G T A C A T G T C 900
DB 841 A T T C C G T A A A G G T A A A A A T T C A A T G A A A C A C A A A C A C A C A A G T T G T A C A T G T C 900
QY 901 C A T A A C T A C G A G C C A C T T C C A A C C A A A T G G T A A T C G T A T T A T T A T G C G T C T A T G G T T G 960
DB 901 C A T A A C T A C G A G C C A C T T C C A A C C A A A T G G T A A T C G T A T T A T T A T G C G T C T A T G G T T G 960
QY 961 G A C T G T T G A C C C T C T T G T C G A A T A T T A T T A T T G T C G A C A G T T G G G G C A A C T G C G T C C A C C 1020
DB 961 G A C T G T T G A C C C T C T T G T C G A A T A T T A T T A T T G T C G A C A G T T G G G G C A A C T G C G T C C A C C 1020
QY 1021 A G G A C A A C G C T A A G G G G A C C A C T A C T G T T G A T G G A G A A C A T A T G A T A T C T A C G A A C 1080
DB 1021 A G G A C A A C G C T A A G G G G A C C A C T A C T G T T G A T G G A G A A C A T A T G A T A T C T A C G A A C 1080
QY 1081 T C T T A G A G T C A A T C A A C C C T C A T T A A G G G A T T G C C A C A T T T A A A C A A T A T T G A G T G T 1140
DB 1081 T C T T A G A G T C A A T C A A C C C T C A T T A A G G G A T T G C C A C A T T T A A A C A A T A T T G A G T G T 1140
QY 1141 T C G A A G A T C G A A A C G C A G C A G T G G C A C G A T T T C T G C A G C A A C C A C T T T A G A G C G T G G A 1200
DB 1141 T C G A A G A T C G A A A C G C A G C A G T G G C A C G A T T T C T G C A G C A A C C A C T T T A G A G C G T G G A 1200
QY 1201 A A A C T T A G G A T A G A A T A T G G G G A A A T G T A G A A G T C G C G T T A C T G T A G A A G C T A T C A 1260
DB 1201 A A A C T T A G G A T A G A A T A T G G G G A A A T G T A G A A G T C G C G T T A C T G T A G A A G C T A T C A 1260
QY 1261 A A G T A G C G A A G T G C T A A T G T A T A T A G C A A T A C A C T A A G A A T T A A C G T A A C C C T C T C T C 1320
DB 1261 A A G T A G C G A A G T G C T A A T G T A T A T A G C A A T A C A C T A A G A A T T A A C G T A A C C C T C T C T C 1320
QY 1321 A A C T A T T A G T A A T G A C A G A G A C A T A A C T T T G G A T A A A A A C A A T T A A A A A T C C T T A T C T C T 1380
DB 1321 A A C T A T T A G T A A T G A C A G A G A C A T A A C T T T G G A T A A A A A C A A T T A A A A A T C C T T A T C T C T 1380
QY 1381 T T C G G T C A G T T C A T T A T T T C A A T A A C C T C C G G T G G A T C T T T C A A C G G G A G G 1440
DB 1381 T T C G G T C A G T T C T C A T T A T T T T C A A A T A A C C T C C G G T T G G A T C T T T T C A A C G G G A G G 1440
QY 1441 T T T T A T T G G A A G G T T A A G T A T A T A C T C C G A T T C C A T C C A G A G A A T G C T T G A A A C A 1500
DB 1441 T T T T A T T G G A A G G T T A A G T A T A T A C T C C G A T T C C A T C C A G A G A A T G C T T G A A A C A 1500
QY 1501 C C T C C G T C A C T A G 1513
DB 1501 C C T C C G T C A C T A G 1513
RESULT 2
AAV30255
ID AAV30255 standard; DNA; 871 BP.
XX
AC AAV30255;
XX
DT 17-OCT-2003 (revised)
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 18-AUG-1998 (first entry)
XX
DE DNA encoding a *Bacillus agaradherens* xylanolytic enzyme.
XX
KW Xylanolytic enzyme; *Bacillus agaradherens* NCIMB 40482; breakdown;
KW agricultural waste; alcohol fuel; enzymatic treatment; animal feed;
KW release; free pentose sugar; dissolving pulp; cellulose; bio-bleaching;
KW wood pulp; lignocellulosic material; animal feed additive; ss.
XX
OS *Bacillus agaradherens*.
XX
FH Key Location/Qualifiers

PT of paper pulp, animal feeds and in bakery goods.

XX Claim 9; Page 54-55; 94pp; English.

XX A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was isolated from a gene library of *Bacillus* sp. 720/1 (LMG P-14798). The sequence (AAT16103) for the complete gene including 5' and 3' untranslated sequences was also obtd. The gene may be incorporated into a vector and expressed from either its own promoter or from the *Bacillus* *pmlus* PRL B12 promoter (see AAR9396), and used for prodn. of recombinant thermostable xylanase in transformed hosts, pref. *Bacillus* licheniformis or *B. pumilus*. The enzyme is useful in the paper-pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 744 BP; 246 A; 144 C; 160 G; 194 T; 0 U; 0 Other;

Query Match: 49.2%; Score 744; DB 2; Length 744;

Best Local Similarity 100.0%; Pred. No. 1.7e-165;

Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	620	ATGAGCAAAAGAAATGACGTTGATTTAGCTTTTATGTTTGTGCTTAACTTAACTTA	679
DB	1	ATGAGCAAAAGAAATGACGTTGATTTAGCTTTTATGTTTGTGCTTAACTTAACTTA	60
QY	680	CCTGCAGAAATTAATTCAGGACAAATTCGTCACGCAATTCATTTGGCAACACCATGGC	739
DB	61	CCTGCAGAAATTAATTCAGGACAAATTCGTCACGCAATTCATTTGGCAACACCATGGC	120
QY	740	TATGATTTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCAATCATGGC	799
DB	121	TATGATTTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCAATCATGGC	180
QY	800	GCTAGCTTCAGTCCCAATGGAACATGTTTACACATATTTTCGTTAAAGTAAAAA	859
DB	181	GCTAGCTTCAGTCCCAATGGAACATGTTTACACATATTTTCGTTAAAGTAAAAA	240
QY	860	TTCAATGAAACAAACACCAACCAATGTTGTAACATGTCATTAATCTACGAGCCAAAC	919
DB	241	TTCAATGAAACAAACACCAACCAATGTTGTAACATGTCATTAATCTACGAGCCAAAC	300
QY	920	TTCCAAACCAATGTAATGCGTATTTATGCGTCTATGTTGACCTTTGACCTTTGTC	979
DB	301	TTCCAAACCAATGTAATGCGTATTTATGCGTCTATGTTGACCTTTGACCTTTGTC	360
QY	980	GAATATTTATGTCGACAGTTGGGCACTGGCTCCACAGGACGACGCTTAAGGGG	1039
DB	361	GAATATTTATGTCGACAGTTGGGCACTGGCTCCACAGGACGACGCTTAAGGGG	420
QY	1040	ACCATCACTGTTGATGGAGAAACATATGATATCTACGAGCTCTTTAGAGTCAATCAACC	1099
DB	421	ACCATCACTGTTGATGGAGAAACATATGATATCTACGAGCTCTTTAGAGTCAATCAACC	480
QY	1100	TCCATTAAGGGGATTCACATTTTAAACATATTCGAGTGTTCGAAGATCGAAACGACG	1159
DB	481	TCCATTAAGGGGATTCACATTTTAAACATATTCGAGTGTTCGAAGATCGAAACGACG	540
QY	1160	AGTGGCAGCATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAACCTTAGGGATGATATG	1219
DB	541	AGTGGCAGCATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAACCTTAGGGATGATATG	600
QY	1220	GGGAAATGATGAAGTCCGCTTACTGTAGAAGGCTATCAAAAGTAGCGGAGTCTTAAT	1279
DB	601	GGGAAATGATGAAGTCCGCTTACTGTAGAAGGCTATCAAAAGTAGCGGAGTCTTAAT	660
QY	1280	GTAATAGCAATACATTAAGATTAACCGTAAACCTCTCTCACTATTAGTAATGACGAG	1339
DB	661	GTAATAGCAATACATTAAGATTAACCGTAAACCTCTCTCACTATTAGTAATGACGAG	720
QY	1340	AGCATAACTTTTGGATAAAAAACAAT	1363
DB	721	AGCATAACTTTTGGATAAAAAACAAT	744

RESULT 4

AAV13067 standard; DNA; 744 BP.

XX AAV13067;

DT 19-MAY-1998 (first entry)

XX Glycosyl hydrolase family 11 xylanase DNA derived from *Bacillus* sp.

XX *Bacillus* sp; xylanase; glycosyl hydrolase family 11; isolation;

KW microorganism; identification; ss.

XX *Bacillus* sp.

PH Key Location/Qualifiers

FT CDS 1..747

FT /*tag= a

FT /product= "glycosyl hydrolase family 11 xylanase"

XX WO9743409-A2.

XX 20-NOV-1997.

XX 12-MAY-1997; 97WO-DK000216.

XX 10-MAY-1996; 96DK-00000562.

XX (NOVO) NOVO-NORDISK AS.

XX Dalboge H, Diderichsen B, Sandal T, Kauppinen S;

DR WPI; 1998-008878/01.

DR P-PSDB; AAW44262.

XX Isolating novel DNA sequences from microorganisms - without the need for culturing the microorganism.

XX Example 1; Page 31-32; 72pp; English.

CC The present sequence encodes a polypeptide with xylanase activity used in an example of the present invention. The present invention describes a novel method for providing a novel DNA sequence encoding a polypeptide from a microorganism with an activity of interest. The method comprises: (i) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence and a 3' structural gene sequence; (iii) expressing the resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide with the activity of interest or a related activity; and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for identification and isolation of sequences from microorganisms without having to cultivate and isolate the microorganism

XX Sequence 744 BP; 249 A; 146 C; 157 G; 192 T; 0 U; 0 Other;

Query Match 47.2%; Score 713.6; DB 2; Length 744;

Best Local Similarity 97.4%; Pred. No. 2.5e-158;

Matches 725; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY	620	ATGAGCAAAAGAAATGACGTTGATTTAGCTTTTATGTTTGTGCTTAACTTAACTTA	679
DB	1	ATGAGCAAAAGAAATGACGTTGATTTAGCTTTTATGTTTGTGCTTAACTTAACTTA	60
QY	680	CCTGCAGAAATTAATTCAGGACAAATTCGTCACGCAATTCATTTGGCAACACCATGGC	739
DB	61	CCTGCAGAAATTAATTCAGGACAAATTCGTCACGCAATTCATTTGGCAACACCATGGC	120
QY	740	TATGATTTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCAATCATGGC	799
DB	121	TATGATTTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCAATCATGGC	180

QY 800 GGTACGTTTCAGTCCCAATGGAACAAATGTTAAACAATATTTTCGTAAGGTAAAAA 859
 DB |||||
 QY 181 GGTACGTTTCAGTCCCAATGGAACAAATGTTAAACAATATTTTCGTAAGGTAAAAA 240
 DB |||||
 QY 860 TTCAATGAAACACAAACACCAACAAAGTTGGTAACATCTCCATAAATACCGAGCCAA 919
 DB |||||
 QY 241 TTCAATGAAACACAAACACCAACAAAGTTGGTAACATCTCCATAAATACCGAGCCAA 300
 DB |||||
 QY 920 TTCCAAACCAATGTTGTAATCGGTATTTATCGGTCTATGGTGGAGTTCGACCTCTTGT 979
 DB |||||
 QY 301 TTCCAGCAACCGAATCGTATTTATCGGTCTATGGTGGAGTTCGACCTCTTGT 360
 DB |||||
 QY 980 GAATATTATTTGTCACAGTTGGGCAATGCGCTCCACAGGAGCAACGCTTAAGGG 1039
 DB |||||
 QY 361 GAATATTATTTGTCATAGTTGGGCAATGCGCTCCACAGGAGCAACGCTTAAGGG 420
 DB |||||
 QY 1040 ACCATCACTGTTGATCGGAGCAATATGATATCTACGAGCTCTTAGAGTCAATCAACCC 1099
 DB |||||
 QY 421 ACCATCACTGTTGATCGGAGCAATATGATATCTATGAAACTCTTAGAGTCAATCAGCC 480
 DB |||||
 QY 1100 TCCATTAAGGGGATTCGCACATTTAAACAATTTGGAGTGTTCGAGATCGAAGCGACG 1159
 DB |||||
 QY 481 TCCATTAAGGGGATTCGCACATTTAAACAATTTGGAGTGTTCGAGATCGAAGCGACG 540
 DB |||||
 QY 1160 AGTGGCAGGATTTCTGTGACGACCACTTTAGAGCGTGGGAACTTAGGGATGAATATG 1219
 DB |||||
 QY 541 AGTGGCAGGATTTCTGTGACGACCACTTTAGAGCGTGGGAACTTAGGGATGAATATG 600
 DB |||||
 QY 1220 GGGAAATGTATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAAAGTGTAA 1279
 DB |||||
 QY 601 GGGAAATGTATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAAAGTGTAA 660
 DB |||||
 QY 1280 GTATATAGCAATACACTAAGAAATTAACGGTAAACCTCTCAACTATTAGTAATGACA 1339
 DB |||||
 QY 661 GTATATAGCAATACACTAAGAAATTAACGGTAAACCTCTCAACTATTAGTAATGACA 720
 DB |||||
 QY 1340 AGCATAACTTTGATTAACCAAT 1363
 DB |||||
 QY 721 AGCATAACTTAGTAACCAAT 744
 DB |||||

RESULT 5

AAQ92878
 ID AAQ92878 standard; DNA; 744 BP.
 XX AC
 XX AAQ92878;
 DT 16-OCT-2003 (revised)
 DT 12-FEB-1996 (first entry)
 XX
 DE Thermostable alkaline endo-1,4-beta-D-xylanase gene.
 XX
 KW thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning;
 KW polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper; pulp;
 KW bleaching; ds.
 XX
 OS Bacillus sp; 1-43-3 (CBS 672.93).
 XX
 XX WO9518219-A1.
 PN
 XX
 XX 06-JUL-1995.
 PD
 XX
 XX 23-DEC-1994; 94WO-EP004312.
 XX
 XX 24-DEC-1993; 93EP-00203694.
 XX
 XX (KONN) GIST-BROCADES NV.
 PA
 XX Van Solingen P, Williams DP, Iverson S, Farrell RL, Herbes WT;
 PI Van Der Kleij WA, Herweijer MA, Van Beekhoven RPWC, Quax WJ;
 PI Goedegebuur F, Jones BE;
 XX
 XX WPI; 1995-246385/32.
 DR

DR P-PSDB; AAR76551.
 XX Novel xylanase enzyme active at high pH - useful in paper and pulp prodn.
 PT processes.
 PT
 XX Claim 4; Page 42-43; 54pp; English.
 XX
 CC The sequence encodes an alkaline endo-1,4-beta-D-xylanase (G-type) from
 CC Bacillus sp. 1-43-3. Fragments of the sequence (e.g. the internal
 CC fragments given in AAQ92878 and AAQ92877) may be amplified by polymerase
 CC chain reaction, e.g. using primers with sequences AAQ92866, AAQ92867,
 CC AAQ92868 and AAQ92869. The DNA may be cloned in Escherichia coli using a
 CC plasmid vector for recombinant xylanase production. The xylanase may be
 CC used in the paper and pulp industries, where it produces an increase in
 CC ISO brightness of softwood pulp of at least 1.0 over non-enzymatically
 CC treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg C.
 CC The enzyme may be used in production of paper, board and fluff pulp, and
 CC has low cellulase activity. The increased brightness produced using the
 CC xylanase allows reduction in the amount of bleaching chemicals used.
 CC (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SX Sequence 744 BP; 248 A; 145 C; 159 G; 192 T; 0 U; 0 Other;
 SX
 Query Match 44.5%; Score 673.6; DB 2; Length 744;
 Best Local Similarity 95.7%; Pred. No. 6.8e-149;
 Matches 714; Conservative 0; Mismatches 29; Indels 3; Gaps 2;
 QY 620 ATGACGACAAAGAAATTCAGCTTGAATTTTAGCTTTTGTAGTTTGTTCACCTTA 679
 DB 1 ATGACGACAAAGAAATTCAGCTTGAATTTTAGCTTTTGTAGTTTGTTCACCTTA 57
 QY 680 CCTGACGAAATTAATTCAGGCAAAATTCGTCACGCAATTCATTTGGCAACCAATGCG 739
 DB 58 CTGCAAGATTAAGTCAGGCAAAATTCGTCACGCAATTCATTTGGCAACCAATGCG 117
 QY 740 TATGATTTATGAATTTTGGAAAGATAGCGTGTCTGGGCAATGATTTCTCAATCATG 799
 DB 118 TATGATTTATGAATTTTGGAAAGATAGCGTGTCTGGGCAATGATTTCTCAATCATG 177
 QY 800 GGTACGTTTCAGTCCCAATGGAACAAATGTTAAACAATATTTTCGTAAGGTAAAAA 859
 DB 178 GGTACGTTTCAGTCCCAATGGAATTAATGTTAAACAATATTTTCGTAAGGTAAAAA 237
 QY 860 TTCAATGAAACACAAACACCAACAAAGTTGGTAACATCTCCATAAATACCGAGCCAA 919
 DB 238 TTCAATGAAACACAAACACCAACAAAGTTGGTAACATCTCCATAAATACCGAGCCAA 297
 QY 920 TTCCAAACCAATGTTGTAATCGGTATTTATCGGTCTATGGTGGAGTTCGACCTCTTGT 979
 DB 298 TTCCAGCAACCGAATCGTATTTATCGGTCTATGGTGGAGTTCGACCTCTTGT 357
 QY 980 GAATATTATTTGTCACAGTTGGGCAATGCGCTCCACAGGAGCAACGCTTAAGGG 1039
 DB 358 GAATATTATTTGTCACAGTTGGGCAATGCGCTCCACAGGAGCAACGCTTAAGGG 417
 QY 1040 ACCATCACTGTTGATCGGAGCAATATGATATCTACGAGCTCTTAGAGTCAATCAACCC 1099
 DB 418 ACCATCACTGTTGATCGGAGCAATATGATATCTATGAAACTCTTAGAGTCAATCAGCC 477
 QY 1100 TCCATTAAGGGGATTCGCACATTTAAACAATTTGGAGTGTTCGAGATCGAAGCGACG 1159
 DB 478 TCCATTAAGGGGATTCGCACATTTAAACAATTTGGAGTGTTCGAGATCGAAGCGACG 537
 QY 1160 AGTGGCAGGATTTCTGTGACGACCACTTTAGAGCGTGGGAACTTAGGGATGAATATG 1219
 DB 538 AGTGGCAGGATTTCTGTGACGACCACTTTAGAGCGTGGGAACTTAGGGATGAATATG 597
 QY 1220 GGGAAATGTATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAAAGTGTAA 1279
 DB 598 GGGAAATGTATGAAGTCCGCTTACTGTAGAGGCTATCAAGTAGCGGAAAGTGTAA 657
 QY 1280 GTATATAGCAATACACTAAGAAATTAACGGTAAACCTCTCAACTATTAGTAATGACA 1339
 DB |||||

Db 658 GTATATAGCAATACACTAAGAATTACGGAAACCCCTCTCTCACTATTAGTAATAACGAG 717

QY 1340 AGCAATACTTTGGATGATAAAACAATTA 1365

Db 718 AGCAATACTCTAGATAAAACAATTA 743

RESULT 6

AAT16101

ID AAT16101 standard; DNA; 663 BP.

XX AAT16101;

DT 16-OCT-2003 (revised)

DT 15-MAY-1996 (first entry)

XX Xylanase gene.

XX Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking; ss.

XX Bacillus sp; strain 710/1 (LMG P-14798).

XX Key Location/Qualifiers

FT mat_peptide 1..663

FT /*tag= a

FT /BC_number= "3.2.1.8"

XX AU9525086-A.

XX 08-FEB-1996.

XX 19-JUL-1995; 95AU-00025086.

PR 26-JUL-1994; 94BE-00000706.

PR 17-MAY-1995; 95BE-00000448.

XX (SOLV) SOLVAY SA.

XX De Buyl E, Lahaye A, Ledoux P, Detroz R;

XX WPI; 1996-117341/13.

XX P-PSDB; AAR92053.

XX Bacillus derived xylanase active over wide pH range - used in treatment of paper pulp, animal feeds and in bakery goods.

XX Claim 30; Page 50-51; 94pp; English.

CC A DNA sequence (AAT16101) coding for a thermostable mature xylanase (AAR92053) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). Sequences were also obtd. (see AAT16102 and AAT16103) for the xylanase precursor and for the complete gene including 5' and 3' untranslated sequences. DNA coding for the mature enzyme may be incorporated into a vector and expressed from either its own promoter or from the Bacillus pumilus PRL B12 promoter (AAR73996), and used for prodn. of recombinant xylanase in transformed hosts, pref. Bacillus licheniformis or B. pumilus. The enzyme is useful in the paper-pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 663 BP; 220 A; 131 C; 146 G; 166 T; 0 U; 0 Other;

XX Query Match 43.8%; Score 663; DB 2; Length 663;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-146; Indels 0; Gaps 0;

XX Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 CAAATCGTCACCGACAATTCATTCGCAACACACGATGGCTATGATTGAATTTGGAAA 760

Db 1 CAAATCGTCACCGACAATTCATTCGCAACACACGATGGCTATGATTGAATTTGGAAA 60

QY 761 GATACGGTGGCTCTGGGACATGATTCTCATCATGGCGGTACGTTCAAGTCCCAATGG 820

Db 61 CATACGGTGGCTCTGGGACATGATTCTCAATCATGGCGGTACGTTCAAGTCCCAATGG 120

QY 821 AACATGTTAAACAACATATTATTCCGTAAGAGTAAAAAATTCATGAACAACAACACAC 880

Db 121 AACATGTTAAACAACATATTATTCCGTAAGAGTAAAAAATTCATGAACAACAACACAC 180

QY 881 CAACAAGTTGGTAACATGTCATAAACTACGGAGCAACTTCCCAACCAAAATGGTAATCGG 940

Db 181 CAACAAGTTGGTAACATGTCATAAACTACGGAGCAACTTCCCAACCAAAATGGTAATCGG 240

QY 941 TATTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTATTGTGACAGT 1000

Db 241 TATTATGCGTCTATGTTGGACTGTTGACCCCTCTTGTGCAATATTATTGTGACAGT 300

QY 1001 TGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCATCATCTGTTGATGGAGGA 1060

Db 301 TGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCATCATCTGTTGATGGAGGA 360

QY 1061 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAGGGGATTCGCCACA 1120

Db 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAGGGGATTCGCCACA 420

QY 1121 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACG 1180

Db 421 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACG 480

QY 1181 AACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATGGGAAATCTATGAAGTCCGCG 1240

Db 481 AACCACTTTAGAGCGTGGGAAACCTTAGGGATGAATATGGGAAATCTATGAAGTCCGCG 540

QY 1241 CTTACTGTAGAAGGCTATCAAAAGTAGCGGAAGTCTTAATGTATATAGCAATACACTAAGA 1300

Db 541 CTTACTGTAGAAGGCTATCAAAAGTAGCGGAAGTCTTAATGTATATAGCAATACACTAAGA 600

QY 1301 ATTAACGTAACCCCTCTCTCACTATTAGTAATGACGAGACATACTTTGGATAAAAAC 1360

Db 601 ATTAACGTAACCCCTCTCTCACTATTAGTAATGACGAGACATACTTTGGATAAAAAC 660

QY 1361 AAT 1363

Db 661 AAT 663

RESULT 7

AAV13074

ID AAV13074 standard; DNA; 747 BP.

XX AAV13074;

DT 19-MAY-1998 (first entry)

DE Xylanase activity positive clone DNA SEQ ID NO:11.

XX Bacillus sp; xylanase; glycosyl hydrolase family 11; isolation; microorganism; identification; hybrid DNA; ss.

OS Synthetic.

OS Bacillus sp.

XX Key Location/Qualifiers

FT CDS 1..747

FT /*tag= a

FT /product= "positive clone for xylanase activity"

XX W09743409-A2.

XX 20-NOV-1997.

XX 12-MAY-1997; 97WO-DK000216.

XX 10-MAY-1996; 96DK-00000562.

XX (NOVO) NOVO-NORDISK AS.

XX Dalboe H, Diderichsen B, Sandal T, Kauppinen S;
 XX WPI; 1998-008878/01.
 XX Isolating novel DNA sequences from microorganisms - without the need for
 XX culturing the microorganism.
 XX Example 1; Page 35; 72pp; English.
 XX The present sequence represents a positive clone for xylanase activity
 XX from an example of the present invention. The present invention describes
 XX a novel method for providing a novel DNA sequence encoding a polypeptide
 XX from a microorganism with an activity of interest. The method comprises:
 XX (i) PCR amplification of the DNA with PCR primers with homology to (a)
 XX known gene(s) encoding a polypeptide with an activity of interest; (ii)
 XX linking the obtained PCR product of a 5' structural gene sequence and a
 XX 3' structural gene sequence; (iii) expressing the resulting hybrid DNA
 XX sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide
 XX with the activity of interest or a related activity; and (v) isolating
 XX the hybrid DNA sequence identified in step (iv). This method provides for
 XX identification and isolation of sequences from microorganisms without
 XX having to cultivate and isolate the microorganism
 XX
 XX Sequence 747 BP; 236 A; 168 C; 154 G; 189 T; 0 U; 0 Other;
 XX
 XX Query Match 39.0%; Score 590.2; DB 2; Length 747;
 XX Best Local Similarity 86.9%; Pred. No. 3.2e-129;
 XX Matches 649; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
 XX
 QY 620 ATGAGCAAAAGAAATGACGTTGATTTAGCTTTTGTAGCTTTTGTGCACTTAACCTTA 679
 DB 1 ATGAGCAAAAGAAATGACGTTGATTTAGCTTTTGTAGCTTTTGTGCACTTAACCTTA 60
 QY 680 CTGCGAAGAAATTAATCAGGCAAAATCGTCACGCAATTCATTCGCAACCAACGATGCG 739
 DB 61 CTGCGAAGAAATTAATCAGGCAAAATCGTCACGCAATTCATTCGCAACCAACGATGCG 120
 QY 740 TATGATTAATGATTTGGAAAGATAGCGGTGCTCTGGGACAAATGATTCATCATGCG 799
 DB 121 TATGATTAATGATTTGGAAAGATAGCGGTGCTCTGGGACAAATGATTCATCATGCG 180
 QY 800 GGTACGTTGAGTCCCAATGGAACAATGTTAAACAATATTATTCGTAAGGTAAGAAA 859
 DB 181 GGTACGTTGAGTCCCAATGGAACAATGTTAAACAATATTATTCGTAAGGTAAGAAA 240
 QY 860 TTCATGAAACAAACACACCAACCAAGTTGGTAACATGTCCATAAACTACGAGCAAC 919
 DB 241 TTCATGAAACAAACACACCAACCAAGTTGGTAACATGTCCATAAACTATGCGCAAC 300
 QY 920 TTCACCAACCAATGATGATTTATGCGTCTATGTTGGTGGTGGTGGTGGTGGTGGTGGT 979
 DB 301 TTCACCAACCAATGATGATTTATGCGTCTATGTTGGTGGTGGTGGTGGTGGTGGTGGT 360
 QY 980 GAATATTAATTCGCAAGTTCGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCA 1039
 DB 361 GAATATTAATTCGCAAGTTCGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCA 420
 QY 1040 ACCATCACTGTCATGAGGAAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 1099
 DB 421 ACCATCACTGTCATGAGGAAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480
 QY 1100 TCCATTAAGGGGATGCGCAATTTAAACAATATTGAGATGTTTGAAGATCGAAACGACG 1159
 DB 481 TCCATTAAGGGGATGCGCAATTTAAACAATATTGAGATGTTTGAAGATCGAAACGACG 540
 QY 1160 AGTGGACAGATTTCTGACACCACTTTAGAGCGTGGGCACTTAGGAGTGAATATG 1219
 DB 541 AGCGGCACTGCTACTACGCAAAACCACTTTAATGCTCGGGCTGCTCTTGGCATGAATG 600
 QY 1220 GGGAAATGATGAGTGGCGCTTACTGTAGAGGCTTATCAAAAGTACGCGAAGTCTAAT 1279
 DB 601 GGTGATTCATTTACAGATCTCTGTTACTGAGGGCTACCAATCTACCGGAAGTCTAAT 660

QY 1280 GTATATAGCAATACACTAAGAAATTAACGGTAACCTCTCTCACTATTAGTAATGACGAG 1339
 DB 661 GTATATAGCAATACACTAAGAAATTAACGGTAACCTCTCTCACTATTAGTAATGACGAG 720
 QY 1340 AGCAATACTTTGGATAAAACAATAA 1366
 DB 721 AGCAATACTCTAGATAAAACAATAA 747
 XX
 XX RESULT 8
 XX ADJ34947
 XX ID ADJ34947 standard; DNA; 1068 BP.
 XX AC ADJ34947;
 XX XX
 XX DT 22-APR-2004 (first entry)
 XX DE DNA encoding xylanase from an environmental sample seq id 163.
 XX KW antibacterial; fungicide; thermostable xylanase activity;
 XX KW dough conditioning; beverage production; nutritional supplement;
 KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
 KW fungal infection; coccidiosis; gene; ds.
 XX OS Unidentified.
 XX WO2003106654-A2.
 XX PD 24-DEC-2003.
 XX PF 16-JUN-2003; 2003WO-US019153.
 XX PR 14-JUN-2002; 2002US-0389299P.
 XX (DIVE-) DIVERSA CORP.
 XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
 XX Esteghlalian A;
 XX WPI; 2004-099016/10.
 XX P-PSDB; ADJ34948.
 XX Novel xylanase recombinant polypeptide useful for improving textile
 XX texture, treating paper, eliminating microorganisms.
 XX Claim 1; SEQ ID NO 163; 570pp; English.
 XX The invention describes an isolated or recombinant polypeptide (I),
 XX having 50% or more identity to 190 300-1200 residue amino acid sequences
 XX (S1), given in the specification, over a region of 100 or more residues
 XX and the polypeptide as thermostable xylanase activity. (I) is useful for:
 XX dough conditioning; beverage production; as a nutritional supplement in
 XX animal feed; reducing lignin in a wood or a wood product; and for
 XX eliminating and protecting animals from a microorganism comprising xylan.
 XX The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 XX acid encoding a polypeptide having a xylanase activity which involves
 XX amplification of a template nucleic acid with a primer pair capable of
 XX amplifying (II) or its subsequence. (I) is useful for treating and
 XX preventing bacterial infection and fungal infection e.g. coccidiosis.
 XX This sequence encodes xylanase protein isolated from an environmental
 XX sample.
 XX Sequence 1068 BP; 303 A; 249 C; 279 G; 237 T; 0 U; 0 Other;
 XX
 XX Query Match 26.0%; Score 393; DB 12; Length 1068;
 XX Best Local Similarity 75.2%; Pred. No. 1.1e-82;
 XX Matches 518; Conservative 0; Mismatches 165; Indels 6; Gaps 2;
 XX
 QY 620 ATGAGCAAAAGAAATGACGTTGATTTAGCTTTTGTGCACTTAACCTTA 679
 DB 1 ATGAGCAAAAGAAATGACGTTGATTTAGCTTTTGTGCACTTAACCTTA 60

QY 680 CCTGCAGAAATATTCAGGACAAATCGTCACGCAAAATTCATTTGGCAACACCATGATGCG 739
 Db |||||
 QY 61 CTGCGG---CAGTGATCGGACAGCATCACGCAATTCGGTGGTACGATACGGT 117
 Db |||||
 QY 740 TATGATATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAAATGATTCTCAATCATGCG 799
 Db |||||
 QY 118 TATGACTATGAATCTGGAAGGACAGC---GGGAATGGAATCTATGTTCTCGTAGTGGC 174
 Db |||||
 QY 800 GGTGCTTCAGTGCCCAATGGACAAATGTTGTAACACATATTTCCGTAAGGTAAGAAA 859
 Db |||||
 QY 175 GGTACGTTTCAGTGCCGAGTGAGCAATATCAATAATATTTCTGTTCCGTAAGGCAAGAG 234
 Db |||||
 QY 860 TTCAATGAACACAAACACACAAAGTTGTAACATGTCATAAACTACGAGGCAAC 919
 Db |||||
 QY 235 TTCAATGAGCGCAGACCCATCAGCAATTTGAACATTTCCATTAACCTATGTTGTCAC 294
 Db |||||
 QY 920 TTCCAAACCAATGGTAATCGGTATTTATGCGTCTATGTTGACTGTTGACCCCTTTGTC 979
 Db |||||
 QY 295 TACCAACCAATGGCAATTCGTATTTAACGGTCTATGCTGACGGTTGACCCCTCGTC 354
 Db |||||
 QY 980 GAATATTTATGTCGACAGTTGGGCACTGGCGTCCACAGGAGCAACGCTTAAGGG 1039
 Db |||||
 QY 355 GAATATTTACATTTGATAGCTGGGCGAGCTGGCGTCCGCTGGAGCATCGCAAGGG 414
 Db |||||
 QY 1040 ACCATCACTGTTGATGGAGAAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCC 1099
 Db |||||
 QY 415 ACTGTTAACGTTGACGGAGGACGTATGACATTTATGAGCAACTCGTGTCAACAGCT 474
 Db |||||
 QY 1100 TCCATTAAGGGATTCGCACATTTAAACATATTTGAGTGTTCGAAGATCGAAAGCGACG 1159
 Db |||||
 QY 475 TCCATTAAGGACGCGCAACCTTCAAGCAGTATTTGAGTGTTCGGACGCTCAAAACGGACG 534
 Db |||||
 QY 1160 AGTGGCAGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAACTTAGGGATGATATG 1219
 Db |||||
 QY 535 ACCGAAACCATATCTGTAAGCGAGCACTTTAAGGCTGGGAAATTTGGGATGACCATG 594
 Db |||||
 QY 1220 GGGAAATGTTATGAAGTCGCGCTACTGTAGAGGCTATCAAGTAGCGGAGTGTCTAAT 1279
 Db |||||
 QY 595 GCGAAGATGATGAAGTCGCGCTTACGTTGAGGCTTCAAGGCTTCAAGCAGTGGAGCGCTAAT 654
 Db |||||
 QY 1280 GTATATGCAATACATGAATTAACCG 1308
 Db |||||
 QY 655 GTGTATAGCCATACATGACGATCGCGG 683
 Db |||||

RESULT 9
 AAQ80923
 ID AAQ80923 standard; DNA; 1022 BP.
 AC AAQ80923;
 XX
 XX
 XX 02-AUG-1995 (first entry)
 XX
 XX B. pumilus xylanase gene.
 XX
 XX xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping; biobleaching;
 KW bleaching; Bacillus licheniformis; ss.
 KW
 OS Bacillus pumilus.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..185
 FT /*tag= a
 FT /note= "claim 12"
 FT misc_difference 107
 FT /*tag= b
 FT /note= "base n at position 107 is not identified in the
 FT specification"
 FT 186..869
 FT /*tag= c
 FT 186..266
 FT /*tag= d
 FT sig_peptide
 FT /note= "claim 11"
 FT

mat_peptide 267..866
 /*tag= e
 /EC_number= "3.2.1.8"
 /note= "claim 10"
 GB2279955-A.
 18-JAN-1995.
 15-JUL-1993; 93GB-00014780.
 15-JUL-1993; 93GB-00014780.
 (SOLV) SOLVAY & CIE.
 Amory A, Andre C, De Buyl E, Detroz R, Lahaye A, Ledoux P;
 WPI; 1995-039214/06.
 P-PSDB; AAR68849.
 Purified xylanase from Bacillus pumilus PRL B12 - esp. produced in
 transformed Bacillus licheniformis, and related DNA, vectors, etc., used
 for pre-treatment of wood pulp to reduce chlorine or ozone consumption in
 subsequent bleaching.
 Claim 13; Fig 1a-1b; 97pp; English.
 A Bacillus pumilus PRL B12 (ATCC 55443) gene library was screened for
 recombinant plasmids carrying the xylanase gene. A chromosomal fragment
 obtained from isolate pBPX1 was subcloned and expressed in Escherichia
 coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3AI
 fragment) carried by a selected transformant is given in AAQ80923
 XX
 SQ Sequence 1022 BP; 329 A; 197 C; 229 G; 266 T; 0 U; 1 Other;
 Query Match 18.7%; Score 282.8; DB 2; Length 1022;
 Best Local Similarity 62.1%; Pred. No. 1.1e-56;
 Matches 481; Conservative 0; Mismatches 287; Indels 6; Gaps 2;
 QY 599 AATTAAAGGAGGATGCTTAATGAGACAAAGAAATGAGCTGATGATTTAGCTTTTAA 658
 Db |||||
 QY 165 AAAAAGGAGGAGGATGGAATTTGAAAAGATTTAGGCTGTTGTTGATGCTGT 224
 Db |||||
 QY 659 GTTTGTTTTCACCTAACCTTACCTGACAGAAATTAATTCAGGCACAAATCGTCACGACAAT 718
 Db |||||
 QY 225 ATTGATTTGCTGACATGACGCTGTGCGGCTCATGCGGAACGATTTATGATAT 284
 Db |||||
 QY 719 TCCATTCGCAACCAACGATGGCTATGATTTGAAATTTTGGAAAGATAGCGTGGCTCTGGG 778
 Db |||||
 QY 285 AGGATAGGGACACACAGCGGATACGATTTTGAATTTATGGAAGGATTAC---GGAATACC 341
 Db |||||
 QY 779 ACATGATTTCTCATCATGCGGTACGTTGAGTCCCAATGGAACATGTTAACAACATA 838
 Db |||||
 QY 342 TCGATGACCTCAATAACGCGGGGCAATTTAGTCAAGCTGGAACATATTTGGAATGCC 401
 Db |||||
 QY 839 TTATTCGTAAGGTAAAAAATCAATGAACACAAACACACCAACCAAGTTGGTAAACATG 898
 Db |||||
 QY 402 TTATTTGAAAGGAAGAAGTTGATTCCTAAACTCATCATCAACTTTGGCAACATC 461
 Db |||||
 QY 899 TCCATAAATACGAGGCAACCTTCCAAACCAATTTGTAATCGGTATTTATCGTCTATGGT 958
 Db |||||
 QY 462 TCCATCAACTACAAACGAGCCTTTAACCCGGGGGGAATTCCTATTATTGTCATATGGC 521
 Db |||||
 QY 959 TGGACTGTTGACCTCTTGTGCAATATATATTTGTGACAGTTGGGGCACTGGCGTCCA 1018
 Db |||||
 QY 522 TGGACACAATCTCATTAGCTGAATACATATTGTTGAGTCATGCGGCAATATCGTCCA 581
 Db |||||
 QY 1019 CCAGGAGCAACGCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGAG 1078
 Db |||||
 QY 582 ACAGG---ACGTATAAAGGATCATTTTATGCCGATGGAGGCACATATGACATATGAA 638
 Db |||||
 QY 1079 ACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACATTTAAACATATTTGAGT 1138
 Db |||||

639	ACGTCCTCGTCAATCAGCCTTCATCATCTGGAGAGCGCTACCTTCAACAATATTGGAGT	698
1139	GTTTGAAGATCGAAACGACAGTGGCAGGATTTCTGTGACCAACACCTTTAGACGGTGG	1198
699	GTACGTCAAAACAAACGACAGCGGACCGTCTCGCTCAGTGAGCATTTTAAAAAATGG	758
1199	GAAACTTAGGATGAATATGGGAAATGTATGAAGTGGCGCTTACTGTAGAAGGCTAT	1258
759	GAAAGCTTAGGATGCCAATGGGAAATGTATGAAGTGGCGCTTACTGTAGAAGGCTAT	818
1259	CAAAAGTAGCGGAAGTCTAATGTATATAGCAATACACTAAGAAATTAACGGTAAACCTCTC	1318
819	CGAAGCAACGGAAGTGGGATGTATGACGAATCAGCTGATGATTCGATAAAGCATATG	878
1319	TCAACTATTAGTAATGACGAGACATACTTTGGATAAAAACAATTAATAATCC	1372
879	AAAAAGCCAGCAAAAAATGGCTGGCTTTTCTATGATAATTTTCAACTTCC	932

RESULT 10

ADJ35051

ADJ35051 standard; DNA; 1956 BP.

ADJ35051;

22-APR-2004 (first entry)

DNA encoding xylanase from an environmental sample seq id 267.

antibacterial; fungicide; thermostable xylanase activity;

dough conditioning; beverage production; nutritional supplement;

animal feed; lignin reduction; wood product; xylan; bacterial infection;

fungal infection; coccidiosis; gene; ds.

Unidentified.

WO2003106654-A2.

24-DEC-2003.

16-JUN-2003; 2003WO-US019153.

14-JUN-2002; 2002US-0389299P.

(DIVE-) DIVERSA CORP.

Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;

Esteghlalian A;

WPI; 2004-099016/10.

P-PSDB; ADJ35052.

Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.

Claim 1; SEQ ID NO 267; 570pp; English.

The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning; beverage production; as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplification of a template nucleic acid with a primer pair capable of amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylanase protein isolated from an environmental sample.

Sequence 1956 BP; 614 A; 384 C; 423 G; 535 T; 0 U; 0 Other;

SQ

Query Match	18.3%;	Score 276.6;	DB 12;	Length 1956;
Best Local Similarity	66.2%;	Pred. No. 3.8e-55;		
Matches 415;	Conservative 0;	Mismatches 209;	Indels 3;	Gaps 1;
Qy	688	AATAATTCAGGCACAAATCGTCACGCAATTCATTCGTCGCAACACGATGGCTATGATTA	747	
Db	81	AGTACTCGCCGGCGAATAATTTACGACAATGAGACAGGCACACATGAGGCTACGACTA	140	
Qy	748	TGAATTTTGGAAAGATAGCGGTGCTCTGGGACATGATTCCTCAATCATCGCGGTACGTT	807	
Db	141	TCAGCTCTCGAAAGA---CTACGGAAATACGATTAATGGAACCTTAACGCGGTGGTACTTT	197	
Qy	808	CAGTCCCAATGGAACAATGTTAAACAATATTTTCCGTAAAGTAAAAAATTCATGA	867	
Db	198	TAGTTGTCAATGGAGTAAATATCGGTAAATGCACTATTTAGAAAAGGGAGAAAAATTAATTC	257	
Qy	868	AACACAAACACACCAACCAAGTTGGTAAACATGTCATTAACCTACGAGGACCACTTCCAAC	927	
Db	258	CGACAAAACCTATCAAGAAATTAGGAGATATAGTAGTTGAATATGGCTGTGATTACAATCC	317	
Qy	928	AAATGGTAAATCGGTATTTATCGTCTATGTTGGACTGTTGACCTCTTGTGCAATATTA	987	
Db	318	AAACGGAAATTCCTATTTGTGTGTTTACGGTTGGACAAGAAATCCACTGTTGAATATTA	377	
Qy	988	TATTGTGACAGTTCGGGCAACTGGCGTCCACGAGGACCAACGCTTAAGGGGACCATCAC	1047	
Db	378	CATTGTAGAAAGCTGGGCGAGCTGGCGTCCACCTGGAGCAACACCCAAAGGAACCATCAC	437	
Qy	1048	TGTTGATGGAGGAACATATGATATCTACGAGACTCTTTAGAGTCAATCAACCTCCATTA	1107	
Db	438	AGTGGATGGCGTACTTATGAAATATATGAAACTACCCGGGTAAATCAGCCTTCCATCGA	497	
Qy	1108	GGGGATTCGCACATTTAAACAATATTTGGAGTCTTCGAAAGATCGAAGCAGCAGTGGCAC	1167	
Db	498	TGGAACCTGCGACATTTCCAACAATATTTGGAGTGTTCGTACATCCAAAGAAACAACGGGAAC	557	
Qy	1168	GATTTCCTGTCAGCAACCACTTTTAGAGCGTGGGAAACTTTAGGGATGAATATGGGGAAT	1227	
Db	558	AATATCTGTCATGACATTTTAAACAGTGGGAAAGATGGGCATCGGAATGGGTAAGAT	617	
Qy	1228	GTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAGTACGGAAGTCTAATGTATATAG	1287	
Db	618	GTATGAAGTTGCTCTTACCGTTGAAGTTATCAGAGCAGTGGGTACGCTAATGTATATA	677	
Qy	1288	CAATACACTAAGAAATTAACGGTAAACCC	1314	
Db	678	GAATGAATCAGAATAGGTGCAAAATCC	704	

RESULT 11

ADJ34969

ADJ34969 standard; DNA; 684 BP.

ADJ34969;

22-APR-2004 (first entry)

DNA encoding xylanase from an environmental sample seq id 185.

antibacterial; fungicide; thermostable xylanase activity;

dough conditioning; beverage production; nutritional supplement;

animal feed; lignin reduction; wood product; xylan; bacterial infection;

fungal infection; coccidiosis; gene; ds.

Unidentified.

WO2003106654-A2.

24-DEC-2003.

16-JUN-2003; 2003WO-US019153.

14-JUN-2002; 2002US-0389299P.

(DIVE-) DIVERSA CORP.

Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;

Esteghlalian A;

WPI; 2004-099016/10.

P-PSDB; ADJ35052.

Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.

Claim 1; SEQ ID NO 267; 570pp; English.

The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning; beverage production; as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplification of a template nucleic acid with a primer pair capable of amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylanase protein isolated from an environmental sample.

Sequence 1956 BP; 614 A; 384 C; 423 G; 535 T; 0 U; 0 Other;

SQ

PR 14-JUN-2002; 2002US-0389299P.
 XX (DIVE-) DIVERSA CORP.
 XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
 PI Esteghalian A;
 XX WPI; 2004-099016/10.
 DR P-PSDB; ADJ34970.
 XX Novel xylanase recombinant polypeptide useful for improving textile
 PT texture, treating paper, eliminating microorganisms.
 XX Claim 1; SEQ ID NO 185; 570pp; English.
 XX The invention describes an isolated or recombinant polypeptide (I),
 CC having 50% or more identity to 190 300-1200 residue amino acid sequences
 CC (SI), given in the specification, over a region of 100 or more residues
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
 CC dough conditioning; beverage production; as a nutritional supplement in
 CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 CC acid encoding a polypeptide having a xylanase activity which involves
 CC amplification of a template nucleic acid with a primer pair capable of
 CC amplifying (II) or its subsequence. (I) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.
 CC This sequence encodes xylanase protein isolated from an environmental
 CC sample.
 XX
 XX Sequence 684 BP; 221 A; 129 C; 158 G; 176 T; 0 U; 0 Other;
 SQ
 Query Match 18.1%; Score 274.4; DB 12; Length 684;
 Best Local Similarity 64.6%; Pred. No. 9.5e-55;
 Matches 442; Conservative 0; Mismatches 236; Indels 6; Gaps 2;
 620' ATGACACAAAAGAAATTGACGTTGATTTTATGACCTTTTATGTTTGTTCACCTAACCTTA 679
 Db 1 ATGAATTTGAAAAGATTGAGGCTGTTTGTGATGTGATTTGGATTGTGCTGACACTG 60
 680 CTTGACGAAATTAATTCAGGACCAAAATCGTCACCGCAATTCATGCGCAACACGATGCG 739
 Db 61. ACGGCTGTGCCAGCTCATCGGAAACGATTTATGATAATAGGATAGGACACACAGCGGA 120
 740 TATGATTAATGAATTTTGGAAAGATAGCGTGTGCTCGGACAAATGATTTCTCAATCATGCG 799
 Db 121 TACGATTTGATTAATGAAGATTTACGGAATACCTCG---ATGACACTCAATACGCG 177
 800 GGTACGTTTCAGTCCCAATGGAACAAATGTTTAAACAATATTTATTCGTAAGGTAAAGAAA 859
 Db 178 GGGGCATTTAGTGCAAGCTGGAACAATATTGGAATGCTTATTTGGAAGAGGAAGAG 237
 860 TTCATGAAACACAAACACCAACAAAGTTGGTAAATCATGTCATTAATACGAGCCCAAC 919
 Db 238 TTGATTCACCTAAACATCATCACTTGGCAACATCTCATCACTCAACACGACGCC 297
 920 TTCCAAACCAATGTAATGCGTATTTATGCGTCTATGTTGACGTTTGACCTCTTCTGTC 979
 Db 298 TTTACCCGGGGGAATTCCTATTTATGTTGTTATGCTGACGACAAATCTCCATTAGCT 357
 980 GAATATTAATTTGTCAGACATTTGGGGCAACTGGCGTCCACGAGGACCAACGCTTAAGGGG 1039
 Db 358 GAATACTACATTTGTTGAGTCATGCGGACATATCTGTCACACAGG---AACGTATAAAGGA 414
 1040 ACCATCATCTTTGATGGAGGAACATATGATATCTAGAGACTCTTAGAGTCAATCAACCC 1099
 Db 415 TCATTTTATGCGGATGGAGGACATATGACATATATGAACGCTCCGTTCAATCAGCGCT 474
 1100 TCCATTAAGGGGATGCCACATTTTAAACAATTTGGAGTGTTCGAAGATCGAAACGACG 1159
 Db 475 TCTATCATTTGAGAGCGCTACCTTCAACAAATATTTGAGTGTACGTCAACAAACGACCA 534
 1160 AGTGACACGATTTCTGTGACGAAACCACTTTTAGAGCGTGGGAAACTTAGGGATGAATATG 1219

Db 535 AGCGAACTGTTCCGTCAGTGAGCATTTTAAAAATGGGAAAGCTTAGGCATGCCAATG 594
 Qy 1220 GGGAAATGATGAAGTCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAAGTCTTAAT 1279
 Db 595 GGAATAATGTATGAACAGCATTAATTAAGTGTAGAGGCTACCGAAGCAACGGAAGTCCGAAT 654
 Qy 1280 GTATATAGCAATACACTAAGAATT 1303
 Db 655 GTCATGAGCAATCAGCTGATGATT 678
 RESULT 12
 AAZ51821
 ID AAZ51821 standard; DNA; 2364 BP.
 XX
 AC AAZ51821;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Clostridium stercorarium xylanase A DNA.
 XX
 KW Xylanase A; XynA; cellulosome; feruloyl esterase; phenolic acid esterase;
 KW thermostable; ferulic acid; wheat bran; agricultural byproduct; treat;
 KW grass; paper and pulp industry; feed processing; food additive;
 KW plant cell wall material; degradation; ds.
 XX
 OS Clostridium stercorarium.
 XX
 FH Key Location/Qualifiers
 CDS 440..1978
 FT /*tag= e
 FT /product= "Xylanase A"
 XX
 PN WO200014243-A1.
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99WO-US020304.
 XX
 PR 04-SEP-1998; 98US-0099136P.
 XX
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX
 PI Blum DL, Kataeva I, Li X, Ljungdahl LG;
 XX
 DR WPI; 2000-256991/22.
 XX
 DR P-PSDB; AAY70523.
 XX
 PT New recombinant DNA molecule comprising a sequence encoding feruloyl
 PT esterase protein, useful for treating grasses and other plant materials
 PT used in pulp and paper industries, feed processing and food additives.
 PT
 PS Disclosure; Page 97-99; 105pp; English.
 XX
 CC The present sequence is a DNA encoding xylanase A (XynA) from Clostridium
 CC stercorarium. XynA contains family VI cellulose binding domain (CBD)
 CC which is homologous to the CBD of xylanase Z (XynZ) of Clostridium
 CC thermocellum. XynZ is an enzymatic component of C. thermocellum
 CC cellulosome and has a multi-domain structure which includes a dockerin
 CC domain, a catalytic xylanase domain, a family VI cellulose binding domain
 CC and a domain of unknown function. The unknown domain in the N-terminal
 CC region of XynZ has been found to contain feruloyl (phenolic acid)
 CC esterase which is involved in the degradation of plant cell wall
 CC material. The novel feruloyl esterase is thermostable, easy to purify,
 CC has high temperature optima and stable over a wide pH range. The enzyme
 CC is used for producing ferulic acid from wheat bran or agricultural
 CC byproducts, treating grasses or other plant materials used in the pulp
 CC and paper industries, in feed processing and as a food additive
 XX
 SQ Sequence 2364 BP; 791 A; 428 C; 458 G; 687 T; 0 U; 0 Other;
 Query Match 16.9%; Score 255.6; DB 3; Length 2364;

Best Local Similarity 65.1%; Pred. No. 3 6e-50;
Matches 410; Conservative 0; Mismatches 214; Indels 6; Gaps 2;

QY 688 AATAATTCAGGCACAAATCGTCACCGCAATTCCTATGCGCAACACGATGGCTATGATTA 747
DB 520 AGTACTCGCGGGCGGAATTAATTCAGCAATGAGACAGGCACACATGGAGGCTACGACTA 579
QY 748 TGAATTTTGGAAAGATAGCGGTGCTCTGGGCAATGATTCCTCAATCATGGCGGTACGTT 807
DB 580 TGAGCTCTGGAAGA---CTACGGAATACGATTAATGGAACCTTAACGAGCGGTGACTTT 636
QY 808 CAGTGCCCAATGGAACAAATGTTAAACAACATATATTCCTTAAGGTAAAAATTCATGA 867
DB 637 TAGTTGTCATGAGTAATATCGGTATGCACTATTTAGAAAGGGAGAAATTTAATTC 696
QY 868 AACACAAACACACCAACAGTTGGTAAACATGTCCATAAATACGAGGCAACCTTCAACC 927
DB 697 CGACAAACCTATCAAGAAATAGGAGACATAGTGTGAATATGCTGTGATTACAATCC 756
QY 928 AATGTAATGCGTATTTATGCTCTATGTTGGACTGTTGACCTCTGTGCGAATATTA 987
DB 757 AAACGGAATTCCTATTTGTGTGTTTACGGTTGGACAAGAAATCCACTGTTGAATATTA 816
QY 988 TATTGTCGACAGTTGGGCAACTGGCGTCCACAGGAGCAACGCTTAAGGGGACCATCAC 1047
DB 817 CATTTAGAAAGCTGGGGCAGCTGGCTCCACTGGAGCAACACCCAAAGGAACCATCAC 876
QY 1048 TG---TTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCAT 1104
DB 877 ACAGTGGATGGCAGGTACTTATGAAATATATGAAATCACTACCGGTAAATCAGCTTCCAT 936
QY 1105 TAAGGGATGTCACATTTTAAACAAATATTTGAGTGTTCGAAGTTCGAACGCAACGAGTGG 1164
DB 937 CGATGGAATGCGACATTCACAAATATTTGAGTGTTCGTACATCCAAAGAGAACAGCGG 996
QY 1165 CAGGATTTCTGTCAGCAACCACTTTTAGAGCGTGGGAAAACCTTAGGATGAATATGGGAA 1224
DB 997 AACATATCTGTCAGTCAATTTTAAACAGTGGGAAAGATGGGATCGGATGGTAA 1056
QY 1225 AATGATGAAGTGGCGCTTACTGTAGAGGCTATCAAGCTATCAAGTGGGAAAGTGTCTAATGATA 1284
DB 1057 GATGTATGAATGTCTTCTTACCGTTGAAGTTATCAGAGCAGTGGGTACGCTAATGTATA 1116
QY 1285 TAGCAATACACTAAGAAATTAACGGTAACCC 1314
DB 1117 CAAGATGAATCAGAATAGGTGCAAAATCC 1146

RESULT 13

AAT90972
ID AAT90972 standard; DNA; 1190 BP.

XX AC AAT90972;
XX DT 22-MAY-1998 (first entry)

XX DE Nucleotide sequence encoding an enzyme with xylanase activity.

XX KW xynB gene; xylanase; enzyme; Dictyoglomus thermophilum strain Rt46B.1;
XX KW G-Xylanase; beta -1,4-xylanase activity; activity; thermal stability;
XX KW biological bleaching; cellulose product; paper pulp; ss.

XX OS Dictyoglomus thermophilum.

XX FH Location/Qualifiers
XX FT 67..1149
XX FT CDS

XX FT /*tag= a
XX FT /product= "xylanase"

XX FT 67..138
XX FT /*tag= b

XX FT 139..1146
XX FT /*tag= c

XX FT sig_peptide

XX FT mat_peptide

XX FT

PN WO9736995-A2.
XX 09-OCT-1997.
PD 27-MAR-1997; 97WO-NZ000042.
XX 29-MAR-1996; 96NZ-00286296.
XX (PACI-) PACIFIC ENZYMES LTD.
XX Bergquist PL, Gibbs MD, Morris D;
PI WPI; 1997-503090/46.
XX P-PSDB; AAW30267.
DR Dictyoglomus thermophilum xylanase gene - used for producing thermally
XX stable enzymes for the bleaching of cellulase products, especially paper
XX pulp.
XX Disclosure; Fig 3; 34pp; English.
XX The present sequence represents a RT46B.1 xynB gene and encodes a xylanase
XX enzyme. The present sequence is derived from a gene contained within
XX Dictyoglomus thermophilum strain Rt46B.1. The xylanase is contained
XX within the family of enzymes known as G-Xylanases, and has beta -1,4-
XX xylanase activity. The enzyme has high activity and high thermal
XX stability with optimum activity at 85 degrees Celsius and pH 6.5. The
XX xylanase enzyme is used for the biological bleaching of cellulose
XX products, especially paper pulp. Use of the enzyme ensures that waste
XX streams from the biological bleaching will include less toxic material
XX

SQ Sequence 1190 BP; 386 A; 197 C; 277 G; 330 T; 0 U; 0 Other;
Query Match 14.4%; Score 217.2; DB 2; Length 1190;
Best Local Similarity 59.0%; Pred. No. 3.4e-41;
Matches 413; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 594 AAAAAAATTAAGGAGGAATGCCTAATGAGACAAAGAAATTCAGTTGATTTAGCCT 653

DB 41 AATTAAGTAAGCGGGGTGTAAATGTTCTTAATAAACTTAGTAAGTTGCTTAG 100

QY 654 TTTTATGTTGTTTTCACCTTACCTGTCGAGAAATTAATTCAGGACAAATTCGTACCG 713

DB 101 TCGTACTACTTCTGCGAGTGTATACGCAAGTTAATGCTCAAAAGCTTATAACACTAACAA 160

QY 714 ACAATTCATTCGCAACGACGATGCTATGATTAATTTTGGAAAGATAGCGGTGCT 773

DB 161 GTAATGCAAGCGGTACTTTTGTGCTACTTATGACTATGGAAGATA---CAGGGA 217

QY 774 CTGGGACAAATGATTCATCAATCATGCGGTACGTTTCAGTGCCCAATGGAACAAATGTTAACA 833

DB 218 ATACACCAATGACTGTATACACAGGAAGGTTTAGTGTCTAGTCGAGCAATATAACA 277

QY 834 ACATATATTTCGTAAGGTAAAAATTCATTAAGAAACAAACACACCAACAAAGTTGGTA 893

DB 278 ATGCATTATTACAGACAGGTAAAGTACAA-----CCAAAACTGGCAGTCATTAGGCA 331

QY 894 ACATGTCATAAATACGAGGACCACTTCCAAACCAATGTAATGCTATTTATGCTGCT 953

DB 332 CTATTAGAATCACTTACTCAGGCACATATAATCTTAATGTAATCTCTTCTTATGATCT 391

QY 954 ATGTTGGAGTGTGACCTCTTGTGCAATATTATATTGTCAGACAGTTGGGGCAACTGGC 1013

DB 392 ATGTTGGTCTACTAATCTCTTAGTAGAGTTTACATTGTAGAAAGTTGGGTAATTGGC 451

QY 1014 GTCCACGAGGACACGCTTAAGGGACCACTCTCTGTTGATGAGGAAACATATGATATCT 1073

DB 452 GTCCACGAGTGCACCTCTCTTGGACAGGTTACTATCGACGCTGTACCTATGACATTT 511

QY 1074 ACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTCGCACATTTAAACAATATT 1133

DB 512 ACAGAACTACCCGTTGAATACGCCATCTATTTCGCTACAGCTACTTTTGTATCAATATT 571

XX WPI: 2004-099016/10.
DR P-PSDB; ADJ35012.
XX
PT Novel xylanase recombinant polypeptide useful for improving textile
PT texture, treating paper, eliminating microorganisms.
XX
XX
PS Claim 1: SEQ ID NO 227; 570pp; English.
XX
CC The invention describes an isolated or recombinant polypeptide (I),
CC having 50% or more identity to 190 300-1200 residue amino acid sequences
CC (S1), given in the specification, over a region of 100 or more residues
CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
CC dough conditioning; beverage production; as a nutritional supplement in
CC animal feed; reducing lignin in a wood or a wood product; and for
CC eliminating and protecting animals from a microorganism comprising xylan.
CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
CC acid encoding a polypeptide having a xylanase activity which involves
CC amplification of a template nucleic acid with a primer pair capable of
CC amplifying (II) or its subsequence. (II) is useful for treating and
CC preventing bacterial infection and fungal infection e.g. coccidiosis.
CC This sequence encodes xylanase protein isolated from an environmental
CC sample.
XX
SQ Sequence 747 BP; 174 A; 222 C; 244 G; 107 T; 0 U; 0 Other;
Query Match 11.8%; Score 177.8; DB 12; Length 747;
Best Local Similarity 66.1%; Pred. No. 5.9e-32;
Matches 257; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
QY 893 AACATGTCATTAACCTACGAGCGCAACTTCCCAACCAATGGTAATGCGTATTATGCGTC 952
DB 340 AATCAGACGGTGACCTACAGGCAAACTACCGACCCGACGCAATTCATCCTGTGCGTA 399
QY 953 TATGGTTGGACTGTTGACCCCTCTTGTGCAATATTATATTGTCGACAGTTGGGGCAACTGG 1012
DB 400 TATGGATGCGCGCAAAACCCCTCGTGAATACTACATCGTCGATAGTGGGGCAGCTGG 459
QY 1013 CGTCCACGAGGAGCAACGGCTAAGGGGACCATCCTGTTGATGGAGGACATATGATATC 1072
DB 460 CGCCCGCGGGGGAAACGTCATGGGCACCGTCAACCGGACGGCGGCACCTACGACATC 519
QY 1073 TACGAGACTCTTAGAGTCAATCAACCTCCATTAAAGGGGATTGCCACATTTAAACAATAT 1132
DB 520 TACCGCACCCAGCGCGTCAACAGCCTTCCATCGAAGGCACCAAGACCTTCTATCAATAC 579
QY 1133 TGGAGTGTTCGAAGATCGAAACGACAGTGGCAGCATTTCTGTGAGCAACCACTTTAGA 1192
DB 580 TGGAGCGTTTCGCACTCAGAAGCGCACGAGCGGAACGATCACGGTTGCGGCTCACTTCGAC 639
QY 1193 GCSTGGGAACCTTAGGGATGAATATGGGAAAATGTATGAGTCGGCTTACTGTAGAA 1252
DB 640 GCCTGGGCGCAGAAGGGGATGAACATGGGGAGTCTGTACGAGGTGTCGATGACCGCGAG 699
QY 1253 GGCTATCAAAAGTAGCGGAAGTGCTAATGT 1281
DB 700 GGCTATCAAAAGTAGCGGGACCGCGGACGT 728

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 17:09:58 ; Search time 173.81 Seconds
(without alignments)
6187.359 Million cell updates/sec

Title: US-09-909-207-10
Perfect score: 1513
Sequence: 1 AAATGTAATTGTATATCT.....TGAAACACCTCCGCACTAG 1513

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B-COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A-COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B-COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS-COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1513	100.0	1513	3	US-08-470-953A-10
2	1513	100.0	1513	3	US-08-470-953A-11
3	840.6	55.6	871	1	US-08-698-978-1
4	744	49.2	744	3	US-08-470-953A-4
5	744	49.2	744	3	US-08-470-953A-5
6	713.6	47.2	744	3	US-09-189-060B-1
7	673.6	44.5	744	3	US-08-501-126-18
8	663	43.8	663	3	US-08-470-953A-1
9	663	43.8	663	3	US-08-470-953A-2
10	619	40.9	619	3	US-08-470-953A-12
11	587.2	38.8	744	3	US-09-189-060B-11
12	282.8	18.7	1022	3	US-08-275-526C-1
13	282.8	18.7	1022	3	US-08-275-526C-35
14	282.8	18.7	1022	4	US-09-076-677-1
15	282.8	18.7	1022	4	US-09-076-677-35
16	282.8	18.7	1022	4	US-09-073-055-1
17	282.8	18.7	1022	4	US-09-073-055-35
18	272.8	18.0	681	3	US-08-275-526C-30
19	272.8	18.0	681	3	US-08-275-526C-32
20	272.8	18.0	681	4	US-09-076-677-30
21	272.8	18.0	681	4	US-09-076-677-32
22	272.8	18.0	681	4	US-09-073-055-30
23	272.8	18.0	681	4	US-09-073-055-32
24	255.6	16.9	2364	3	US-09-390-234-23
25	255.6	16.9	2364	4	US-09-603-311-23
26	255	16.9	600	3	US-08-275-526C-26
27	255	16.9	600	3	US-08-275-526C-34

Sequence 26, Appl
Sequence 34, Appl
Sequence 26, Appl
Sequence 34, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 13, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 53, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 2, Appl

28 255 16.9 600 4 US-09-076-677-26
29 255 16.9 600 4 US-09-076-677-34
30 255 16.9 600 4 US-09-073-055-26
31 255 16.9 600 4 US-09-073-055-34
32 255 16.9 600 4 US-09-073-055-34
33 255 16.9 600 4 US-09-073-055-34
34 255 16.9 600 4 US-09-073-055-34
35 255 16.9 600 4 US-09-073-055-34
36 255 16.9 600 4 US-09-073-055-34
37 255 16.9 600 4 US-09-073-055-34
38 255 16.9 600 4 US-09-073-055-34
39 255 16.9 600 4 US-09-073-055-34
40 255 16.9 600 4 US-09-073-055-34
41 255 16.9 600 4 US-09-073-055-34
42 255 16.9 600 4 US-09-073-055-34
43 255 16.9 600 4 US-09-073-055-34
44 255 16.9 600 4 US-09-073-055-34
45 255 16.9 600 4 US-09-073-055-34

ALIGNMENTS

RESULT 1
US-08-470-953A-10
; Sequence 10, Application US/08470953A
; Patent No. 6346407
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; APPLICANT: ERIC DE BUYL
; APPLICANT: PIERRE LEDOUX
; APPLICANT: RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
; TITLE OF INVENTION: and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,953A
; FILING DATE: 6-OCTOBER-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1513 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
; US-08-470-953A-10

Query Match 100.0%; Score 1513; DB 3; Length 1513;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATGGAATTTGTATATCTAATGATAACGAAATCGTCACTGTTTAACTAATCTC 60
 Db 1 AAATGGAATTTGTATATCTAATGATAACGAAATCGTCACTGTTTAACTAATCTC 60

Qy 61 AAACCAATCTCTTTTAAATGCGTAACCGTCAATCTTATCAAGAAACATCTTTT 120
 Db 61 AAACCAATCTCTTTTAAATGCGTAACCGTCAATCTTATCAAGAAACATCTTTT 120

Qy 121 ATAGCAATCTTTCCATTTTGCAGAGCATAAATAATCTTTTCCCTATTTTATCTTCG 180
 Db 121 ATAGCAATCTTTCCATTTTGCAGAGCATAAATAATCTTTTCCCTATTTTATCTTCG 180

Qy 181 CTTTCATCGGTTTAAATTTGTAACCTTTTATTTAGTTTACGTGATGTTCCCTCATTCATC 240
 Db 181 CTTTCATCGGTTTAAATTTGTAACCTTTTATTTAGTTTACGTGATGTTCCCTCATTCATC 240

Qy 241 CATTATCAGAGTTAACGTGAGTCACTTTTTCGGTTCTCAAAATACCTGAAGAAC 300
 Db 241 CATTATCAGAGTTAACGTGAGTCACTTTTTCGGTTCTCAAAATACCTGAAGAAC 300

Qy 301 ATTTATGTCATATTTTCTCAGCGCTCCATAATGGAATATATATCTTTTATACATA 360
 Db 301 ATTTATGTCATATTTTCTCAGCGCTCCATAATGGAATATATATCTTTTATACATA 360

Qy 361 TTAAGTAAATAGTATATATCTTTCGTTATCAAAATGTGAGATAATCTAATGTATCAACA 420
 Db 361 TTAAGTAAATAGTATATATCTTTCGTTATCAAAATGTGAGATAATCTAATGTATCAACA 420

Qy 421 AGCAGCTATCCAAAACACTGATGTTGACCTCTTAAAGAAAGTGTCACTATCTATGA 480
 Db 421 AGCAGCTATCCAAAACACTGATGTTGACCTCTTAAAGAAAGTGTCACTATCTATGA 480

Qy 481 GATAATTTACGATTTCAAAATTTTCAAAATAGTGTGATGGAATAGTTTGAATGTCAACTG 540
 Db 481 GATAATTTACGATTTCAAAATTTTCAAAATAGTGTGATGGAATAGTTTGAATGTCAACTG 540

Qy 541 CTGTGAAAGGAGGTTAGTGTAGTACGTTACCTTACCAAAATAGTTTGAATGTCAACTG 600
 Db 541 CTGTGAAAGGAGGTTAGTGTAGTACGTTACCTTACCAAAATAGTTTGAATGTCAACTG 600

Qy 601 TTAAGAGGAGGATCCCTAATGAGACAAAGAAATGACGTTGATTTAGCTTTTATG 660
 Db 601 TTAAGAGGAGGATCCCTAATGAGACAAAGAAATGACGTTGATTTAGCTTTTATG 660

Qy 661 TTGTTTTCACCTAACCTTACCTGAGAAATATTCAGGCACAAATCGTCACGCAATTC 720
 Db 661 TTGTTTTCACCTAACCTTACCTGAGAAATATTCAGGCACAAATCGTCACGCAATTC 720

Qy 721 CATTTGGCAACCAAGTGTATGATTAATGAAATTTTGGAAAGATAGCGTGTCTGGAC 780
 Db 721 CATTTGGCAACCAAGTGTATGATTAATGAAATTTTGGAAAGATAGCGTGTCTGGAC 780

Qy 781 AATGATTTCTCAATCATGSGGTGACGTTTCAAGTCCCAATGGAACATGTTAAACATATT 840
 Db 781 AATGATTTCTCAATCATGSGGTGACGTTTCAAGTCCCAATGGAACATGTTAAACATATT 840

Qy 841 ATTCGTTAAAGGTAAGAAATTTCAATGAAACACAAACACCAACCAAGTTGTAACATGTC 900
 Db 841 ATTCGTTAAAGGTAAGAAATTTCAATGAAACACAAACACCAACCAAGTTGTAACATGTC 900

Qy 901 CATAACTACGAGCAACTTCCAAACCAATGTAATCGTATTTATCGCTATGTTG 960
 Db 901 CATAACTACGAGCAACTTCCAAACCAATGTAATCGTATTTATCGCTATGTTG 960

Qy 961 GACTGTTGACCTCTTGTGCAATATATATGTCAGAGTTGGGCACTGGCGTCCACC 1020
 Db 961 GACTGTTGACCTCTTGTGCAATATATATGTCAGAGTTGGGCACTGGCGTCCACC 1020

RESULT 2
 US-08-470-953A-11
 ; Sequence 11, Application US/08470953A
 ; Patent No. 6346407
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDREE LAHAYE
 ; APPLICANT: ERIC DE BUYL
 ; APPLICANT: PIERRE LEDOUX
 ; APPLICANT: RENE DETROZ
 ; TITLE OF INVENTION: Xylanase, microorganisms produced it,
 ; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
 ; STREET: 2000 K St., N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,953A
 ; FILING DATE: 6-OCTOBER-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilhem F. Gadiano, Esq.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-40

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: 620..1363
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 701..1363
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 620..700
US-08-470-953A-11

Query Match 100.0%; Score 1513; DB 3; Length 1513;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGAATTTGTATATCTAATGATACGACAAATCGTCACCTGTTTAAACAAATTC 60
DB 1 AAATTGAATTTGTATATCTAATGATACGACAAATCGTCACCTGTTTAAACAAATTC 60
QY 61 AAACCAATCTCTTTAATTTAAGCTAACACCTTGCAATCTTATCAAGAAACATCTTT 120
DB 61 AAACCAATCTCTTTAATTTAAGCTAACACCTTGCAATCTTATCAAGAAACATCTTT 120
QY 121 ATAGGAACCTTCCATTTGCAAGACGATAAATAATCTTTTCCCTATTCTTATCTG 180
DB 121 ATAGGAACCTTCCATTTGCAAGACGATAAATAATCTTTTCCCTATTCTTATCTG 180
QY 181 CCTTGATCGGTTTAAATTTGTAAATCTTTATTTAGTTTACGTGATGTTCCCTCATTCAT 240
DB 181 CCTTGATCGGTTTAAATTTGTAAATCTTTATTTAGTTTACGTGATGTTCCCTCATTCAT 240
QY 241 CATTAATCAAGTTAAGCTAGAGTCACTTTTTCGGTTCCTCAAAAATACCTGAAGAAC 300
DB 241 CATTAATCAAGTTAAGCTAGAGTCACTTTTTCGGTTCCTCAAAAATACCTGAAGAAC 300
QY 301 ATTTATGTCATATTTCTCAGCGCGCTCCATATGGAATATATATATCTTTTATACATA 360
DB 301 ATTTATGTCATATTTCTCAGCGCGCTCCATATGGAATATATATATCTTTTATACATA 360
QY 361 TTAAGTAAATAGTATATATCTCGGTTTATCAAAATGTGAGATAATCTAAATGATCAAA 420
DB 361 TTAAGTAAATAGTATATATCTCGGTTTATCAAAATGTGAGATAATCTAAATGATCAAA 420
QY 421 AGCAGCTATCCAAAAACACATGATGTTGACCTCTTAAAGAAAGTGCTACTATCTATGAAA 480
DB 421 AGCAGCTATCCAAAAACACATGATGTTGACCTCTTAAAGAAAGTGCTACTATCTATGAAA 480
QY 481 GATAATTTCCAGTTTCAAAATTTGAAATAGTGTGATGGAATAGTTTGAATGTCACCTG 540
DB 481 GATAATTTCCAGTTTCAAAATTTGAAATAGTGTGATGGAATAGTTTGAATGTCACCTG 540
QY 541 CTGTGAAGAGGGGTAGGTAGTACCGTAGACTTCAATACCAGAAATAGTTGTAAAAAA 600
DB 541 CTGTGAAGAGGGGTAGGTAGTACCGTAGACTTCAATACCAGAAATAGTTGTAAAAAA 600
QY 601 TTAAGAGGAGGAATGCCATATGAGACAAAAGAAATGACGTGATGTTTACGCTTTTAGT 660
DB 601 TTAAGAGGAGGAATGCCATATGAGACAAAAGAAATGACGTGATGTTTACGCTTTTAGT 660
QY 661 TTGTTTGGCTAACCTTACCTGACGAAATTAATTCAGGCACAAATCGTCACCGCAATTC 720

DB 661 TTGTTTGGCTAACCTTACCTGACGAAATTAATTCAGGCACAAATCGTCACCGCAATTC 720
QY 721 CATTTGGCAACACGATGGCTATGATTAATTTTGGAAAGATAGCGGTGGCTCTGGGAC 780
DB 721 CATTTGGCAACACGATGGCTATGATTAATTTTGGAAAGATAGCGGTGGCTCTGGGAC 780
QY 781 AATGATTTCTCAATCATGGCGGTAGCTTCAGTGGCCCAATGGAAACAATGTTAAACAATATT 840
DB 781 AATGATTTCTCAATCATGGCGGTAGCTTCAGTGGCCCAATGGAAACAATGTTAAACAATATT 840
QY 841 ATTCCGTTAAAGGTAAAAAATTTCAATGAAAAACACCAACCAAGTTGGTAAACATGTC 900
DB 841 ATTCCGTTAAAGGTAAAAAATTTCAATGAAAAACCAACCAAGTTGGTAAACATGTC 900
QY 901 CATAAACTACGGAGCCCAACTTCCAAACCAATGTAATGCGTATTATGCGTCTATGGTTG 960
DB 901 CATAAACTACGGAGCCCAACTTCCAAACCAATGTAATGCGTATTATGCGTCTATGGTTG 960
QY 961 GACTGTTGACCCCTCTTGTGCAATATTATTTGTCAGAGTTGGGCAACTGGCGTCCACC 1020
DB 961 GACTGTTGACCCCTCTTGTGCAATATTATTTGTCAGAGTTGGGCAACTGGCGTCCACC 1020
QY 1021 AGGAGCAACGCTAAAGGGACCATCACTGTTGATGGAGAAACATATGATCTACGAGAC 1080
DB 1021 AGGAGCAACGCTAAAGGGACCATCACTGTTGATGGAGAAACATATGATCTACGAGAC 1080
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DB 1081 TCTTAGAGTCAATCAACCCCTCATTTAAGGGGATTCGCATTTAAACAATATTGGAGTGT 1140
QY 1141 TCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACGAAACCACTTTAGAGCGTGGGA 1200
DB 1141 TCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACGAAACCACTTTAGAGCGTGGGA 1200
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DB 1201 AAACTTAGGGATGAATATGGGGAATAATGATGAAGTTCGCGCTTACTGTAGAAGGCTATCA 1260
QY 1261 AAGTAGCGGAAGTGTCTAATGATATAGCAATACACCTTAAGAAATTAACGGTAACCCCTCTC 1320
DB 1261 AAGTAGCGGAAGTGTCTAATGATATAGCAATACACCTTAAGAAATTAACGGTAACCCCTCTC 1320
QY 1321 AACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAACAATTTAAATAATCTTATCTCT 1380
DB 1321 AACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAACAATTTAAATAATCTTATCTCT 1380
QY 1381 TTCCGTTTCAGTTCTCATTAATTTTCAAAATAACCTCCCGGTTGGATCTTTTCAACGGGAGG 1440
DB 1381 TTCCGTTTCAGTTCTCATTAATTTTCAAAATAACCTCCCGGTTGGATCTTTTCAACGGGAGG 1440
QY 1441 TTTTATTGGAAGGTTAAGTATAGTATCTCCGATTCCATCCAGAGGAATGCTTGAACA 1500
DB 1441 TTTTATTGGAAGGTTAAGTATAGTATCTCCGATTCCATCCAGAGGAATGCTTGAACA 1500
QY 1501 CCTCCGTCACCTAG 1513
DB 1501 CCTCCGTCACCTAG 1513

RESULT 3

US-08-698-978-1
; Sequence 1, Application US/08698978
; Patent No. 5770424
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Dammann, Claus
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Sch lein, Martin
; APPLICANT: Jorgensen, Per Linea
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS OF PRODUCING
; ;
; TITLE OF INVENTION: XYLANOLYTIC ENZYMES

Db	301	TTCCAGCCAAACGGAAATCGTATTTATGCGTCTATGGTGGACTGTCACCCCTTGTGC	360
Qy	980	GAATATTATATTCTGCACAGTTTGGGCGCAACTGSCGTCACACGAGAGCAACGCCCTAAGGGG	1039
Db	361	GAATATTATATTGTGCGATAGTTGGGCGCAACTGCGCTCCACACGAGGGCGACGCCCTAAGGA	420
Qy	1040	ACCATCACTGTTGATGGAGGAACATATGATATCTTACGAGACTCTTTAGAGTCATCAACCC	1099
Db	421	ACCATCACTGTTGATGGAGGAACATATGATATCTATGAAACTCTTTAGAGTCATCAAGCCC	480
Qy	1100	TCATTTAAGGGGATTCGCCACATTTAAACAATATTGGAGTGTTCGAGATCGAAACGCACG	1159
Db	481	TCATTTAAGGGGATTCGCCACATTTAAACAATATTGGAGTGTTCGAGATCGAAACGCACG	540
Qy	1160	AGTGGCAGCATTTCTGTCAGCAACCACTTTTAGAGCGTGGGAAAACTTTAGGGATGAATATG	1219
Db	541	AGTGGCAGCAATTTCTGTGAGCAACCACTTTTAGAGCGTGGGAAAACTTTAGGGATGAACATG	600
Qy	1220	GGGAAATGTATGAAGTCCGCTTACTGTAGAAGGCTATCAAGTAGCGGAAGTGCTAAT	1279
Db	601	GGGAAATGTATGAAGTCCGCTTACTGTAGAAGGCTATCAAGTAGCGGAAGTGCTAAT	660
Qy	1280	GTATATAGCAATACACTAAGAATTTAACGGTAAACCCCTCTCAACTATTAGTAAATGACGAG	1339
Db	661	GTATATAGCAATACACTAAGAATTTAACGGTAAACCCCTCTCAACTATTAGTAAATGACGAG	720
Qy	1340	AGCATCACTTTGGATATAAACCAATTTAAAAATCCTTATCTCTTTTCGTTTCAGTTCTCATTA	1399
Db	721	AGCATCACTCTAGATAAAAAACAATTTAAAAATCCTTATCTCTTTTCGTTTCAGTTCTCATTA	780
Qy	1400	TTTTTCAATAAACCCTCCGGTTCGATCTTTTCCAAACGGGAGGTTTATTTCGAAAGGTTAAG	1459
Db	781	TTTTTCAATAAACCCTCCGGTTCGATCTTTTCCAAACGGGAGGTTTATTTCGAAAGGTTAAG	840
Qy	1460	TATAGTATACTCCGATTCATCCAGAGGAAT	1490
Db	841	TATAGTATACTCCGATTCATCCAGAGGAAT	871

RESULT 4

US-08-470-953A-4

Sequence 4, Application US/08470953A

Patent No. 6346407

GENERAL INFORMATION:

APPLICANT: ANDREE LAHAVE

APPLICANT: ERIC DE BUVL

APPLICANT: PIERRE LEDOUX

APPLICANT: RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: and uses thereof

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE

STREET: 2000 K St., N.W., Suite 200

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,953A

FILING DATE: 6-OCTOBER-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

```

; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
; US-08-470-953A-4

Query Match 49.2%; Score 744; DB 3; Length 744;
Best Local Similarity 100.0%; Pred. No. 4.6e-190; Indels 0; Gaps 0;
Matches 744; Conservative 0; Mismatches 0;

QY 620 ATGAGACAAAGAAATGACGTTGATTTAGCCCTTTTGTAGTTTGTGCTTAACCTTA 679
DB 1 ATGAGACAAAGAAATGACGTTGATTTAGCCCTTTTGTAGTTTGTGCTTAACCTTA 60

QY 680 CTGCGAGAAATAATTCAGGCACAAATCGTCACCGACAATTCATTCGTCGCAACGATGGC 739
DB 61 CTGCGAGAAATAATTCAGGCACAAATCGTCACCGACAATTCATTCGTCGCAACGATGGC 120

QY 740 TATGATTTGAATTTTGGAAAGATAGCGTGGCTCTGGGACATGATTCATCATGTC 799
DB 121 TATGATTTGAATTTTGGAAAGATAGCGTGGCTCTGGGACATGATTCATCATGTC 180

QY 800 GGTACGTTTCAGTGCCCAATGGAACAATGTTAAACAATATTTCCGTAAAGTAAAAA 859
DB 181 GGTACGTTTCAGTGCCCAATGGAACAATGTTAAACAATATTTCCGTAAAGTAAAAA 240

QY 860 TTCAATGAAACACAAACACACCAAGTTGGTAAACATGTCATTAACCTACGAGCAAC 919
DB 241 TTCAATGAAACACAAACACACCAAGTTGGTAAACATGTCATTAACCTACGAGCAAC 300

QY 920 TTCACACCAATGTAATGCTATTTATGCTCTATGTTGGACTGTGACCTCTTGTG 979
DB 301 TTCACACCAATGTAATGCTATTTATGCTCTATGTTGGACTGTGACCTCTTGTG 360

QY 980 GAATATTTATTTGTCAGACGTTGGGCAACTGGGCTCCACGAGCAACGCTTAAGGG 1039
DB 361 GAATATTTATTTGTCAGACGTTGGGCAACTGGGCTCCACGAGCAACGCTTAAGGG 420

QY 1040 ACCATCACTGTTGATGAGGAAACATATGATATCTACGAGACTCTTAGTCAATCAACC 1099
DB 421 ACCATCACTGTTGATGAGGAAACATATGATATCTACGAGACTCTTAGTCAATCAACC 480

QY 1100 TCCATTAAGGGATTCGCACATTTAAACAATTTGGAGTGTTCGAGATCGAAACGACG 1159
DB 481 TCCATTAAGGGATTCGCACATTTAAACAATTTGGAGTGTTCGAGATCGAAACGACG 540

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DB 541 AGTGGCACGATTTCTGTGACCAACCACTTTAGAGCGTGGGAAACCTTAGGATGAATG 600

QY 1220 GGGAAATGATGAAGTTCGCTTATCTGTAGAGGCTATCAAGTAGCGGAAGTCTAAT 1279
DB 601 GGGAAATGATGAAGTTCGCTTATCTGTAGAGGCTATCAAGTAGCGGAAGTCTAAT 660

QY 1280 GTATATAGCAATACACTAAGATTTAAACGTTAAACCTCTCTCACTATTAGTATGACG 1339
DB 661 GTATATAGCAATACACTAAGATTTAAACGTTAAACCTCTCTCACTATTAGTATGACG 720

QY 1340 AGCATAACTTTGGATAAAAAAAT 1363
DB 721 AGCATAACTTTGGATAAAAAAAT 744
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RESULT 5
US-08-470-953A-5
; Sequence 5, Application US/08470953A
; Patent No. 6346407
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; APPLICANT: ERIC DE BUYL
; APPLICANT: PIERRE LEDOUX
; APPLICANT: RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
; TITLE OF INVENTION: and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,953A
; FILING DATE: 6-OCTOBER-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..744
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 82..744
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..81
; US-08-470-953A-5

Query Match 49.2%; Score 744; DB 3; Length 744;
Best Local Similarity 100.0%; Pred. No. 4.6e-190; Indels 0; Gaps 0;
Matches 744; Conservative 0; Mismatches 0;

QY 620 ATGAGACAAAGAAATGACGTTGATTTAGCCCTTTTGTAGTTTGTGCTTAACCTTA 679
DB 1 ATGAGACAAAGAAATGACGTTGATTTAGCCCTTTTGTAGTTTGTGCTTAACCTTA 60

QY 680 CTGCGAGAAATAATTCAGGCACAAATCGTCACCGACAATTCATTCGTCGCAACGATGGC 739
DB 61 CTGCGAGAAATAATTCAGGCACAAATCGTCACCGACAATTCATTCGTCGCAACGATGGC 120

QY 740 TATGATTTGAATTTTGGAAAGATAGCGTGGCTCTGGGACATGATTCATCATGTC 799
DB 121 TATGATTTGAATTTTGGAAAGATAGCGTGGCTCTGGGACATGATTCATCATGTC 180

QY 800 GGTACGTTTCAGTGCCCAATGGAACAATGTTAAACAATATTTCCGTAAAGTAAAAA 859
DB 181 GGTACGTTTCAGTGCCCAATGGAACAATGTTAAACAATATTTCCGTAAAGTAAAAA 240

QY 860 TTCAATGAAACACAAACACACCAAGTTGGTAAACATGTCATTAACCTACGAGCAAC 919
DB 241 TTCAATGAAACACAAACACACCAAGTTGGTAAACATGTCATTAACCTACGAGCAAC 300

QY 920 TTCACACCAATGTAATGCTATTTATGCTCTATGTTGGACTGTGACCTCTTGTG 979
DB 301 TTCACACCAATGTAATGCTATTTATGCTCTATGTTGGACTGTGACCTCTTGTG 360

QY 980 GAATATTTATTTGTCAGACGTTGGGCAACTGGGCTCCACGAGCAACGCTTAAGGG 1039
DB 361 GAATATTTATTTGTCAGACGTTGGGCAACTGGGCTCCACGAGCAACGCTTAAGGG 420

QY 1040 ACCATCACTGTTGATGAGGAAACATATGATATCTACGAGACTCTTAGTCAATCAACC 1099
DB 421 ACCATCACTGTTGATGAGGAAACATATGATATCTACGAGACTCTTAGTCAATCAACC 480

QY 1100 TCCATTAAGGGATTCGCACATTTAAACAATTTGGAGTGTTCGAGATCGAAACGACG 1159
DB 481 TCCATTAAGGGATTCGCACATTTAAACAATTTGGAGTGTTCGAGATCGAAACGACG 540

QY 1160 AGTGGCACGATTTCTGTGACCAACCACTTTAGAGCGTGGGAAACCTTAGGATGAATG 1219
DB 541 AGTGGCACGATTTCTGTGACCAACCACTTTAGAGCGTGGGAAACCTTAGGATGAATG 600

QY 1220 GGGAAATGATGAAGTTCGCTTATCTGTAGAGGCTATCAAGTAGCGGAAGTCTAAT 1279
DB 601 GGGAAATGATGAAGTTCGCTTATCTGTAGAGGCTATCAAGTAGCGGAAGTCTAAT 660

QY 1280 GTATATAGCAATACACTAAGATTTAAACGTTAAACCTCTCTCACTATTAGTATGACG 1339
DB 661 GTATATAGCAATACACTAAGATTTAAACGTTAAACCTCTCTCACTATTAGTATGACG 720

QY 1340 AGCATAACTTTGGATAAAAAAAT 1363
DB 721 AGCATAACTTTGGATAAAAAAAT 744

CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,126
FILING DATE: 29-DEC-1995
CLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0057.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
STRAIN: 1-43-3
INDIVIDUAL ISOLATE: CBS672.93
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
OTHER INFORMATION: /product= "xylanase"
US-08-501-126-18

Query Match	44.5%;	Score 673.6;	DB 3;	Length 744;
Best Local Similarity	95.7%;	Pred. No. 3.6e-171;		
Matches 714;	Conservative	0;	Mismatches 29;	Indels 3; Gaps 2;
QY	620	ATGAGACAAAGAAATTGACGTTGATTTTAGCCCTTTTATGTTTGTGTTGACCTAAACCTTA	679	
DB	1	ATGAGCCAAAGAAATTGACGTTGA--TTAACCTTTTATGTTG--TTTGACCTAAACCTTA	57	
QY	680	CCTGCAGAAATAATTGAGGCACAAATCGTCACCGACAATTCATTTGTCGAACCAAGATGGC	739	
DB	58	CCTGCAAGATAAGTCAGGCACAAATCGTCACCGACAATTCATTTGTCGACCCGCGGTGGT	117	
QY	740	TATGATTATGAAATTTTGGRAAGATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGC	799	
DB	118	TATGATTATGAAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTTCTCAATCATGGC	177	
QY	800	GGTACGTTTCAGTGCCCAATGGAAACAATGTTTAAACAACATATATTTCGTAAAGGTAAAAA	859	
DB	178	GGTACGTTTCAGTGCCCAATGGAATAATGTTTAAACAATATATTTCGTAAAGGTAAAAA	237	
QY	860	TTCAATGAAACACAAACACACCAACAGTTGGTAAACATGTCCATAAATCTACGGAGCAAC	919	
DB	238	TTCAATGAAACACAAACACACCAACAGTTGGTAAACATGTCCATAAATCTATGGCGCAAC	297	
QY	920	TTCCAAACCAATGGTAAATGCGTATTTATGGCTCTATGGTTGGACTGTTGACCCCTCTTGTC	979	
DB	298	TTCCAGCCAAACGGTAATGGTATTTATGGCTCTATGGTTGGACTGTTGACCCCTCTTGTT	357	
QY	980	GAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACAGAGACAAAGCCTTAAGGGG	1039	
DB	358	GAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACAGAGACAAAGCCTTAAGGGA	417	

STRAIN: Bacillus
US-08-470-953A-1

Query Match 43.8%; Score 663; DB 3; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.4e-168;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 701 CAAATCGTCACGACAAATCCATTGGCAACCAAGGATGCTATGATTAATGAAATTTGGAAA 760
DB 1 CAAATCGTCACGACAAATCCATTGGCAACCAAGGATGCTATGATTAATGAAATTTGGAAA 60
QY 761 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGCGCGGTACGTTCAATGCGGCAATGG 820
DB 61 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGCGCGGTACGTTCAATGCGGCAATGG 120
QY 821 AACAAATGTTAAACAAATATTTTCGTAAGGTAAAGGATTAATTAATGAAACACACAC 880
DB 121 AACAAATGTTAAACAAATATTTTCGTAAGGTAAAGGATTAATTAATGAAACACACAC 180
QY 881 CAACAAATGTTAAACAAATGTTTCGTAAGGTAAAGGATTAATTAATGAAACACACAC 940
DB 181 CAACAAATGTTAAACAAATGTTTCGTAAGGTAAAGGATTAATTAATGAAACACACAC 240
QY 941 TATTTATGCGTCTATGTTGGACTGTTGACCCCTTTGTCGAATATTAATTTGTCGACAGT 1000
DB 241 TATTTATGCGTCTATGTTGGACTGTTGACCCCTTTGTCGAATATTAATTTGTCGACAGT 300
QY 1001 TGGGGCAACTGGCGTCCACGAGGACCAAGCTTAAGGGACCATCACTGTTGATGGAGGA 1060
DB 301 TGGGGCAACTGGCGTCCACGAGGACCAAGCTTAAGGGACCATCACTGTTGATGGAGGA 360
QY 1061 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACA 1120
DB 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACA 420
QY 1121 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTCAAG 480
DB 421 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTCAAG 480
QY 1181 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGATATGGGAAAATGATGAAGTCGCG 1240
DB 481 AACCACTTTAGAGCGTGGGAAAACCTTAGGATGATATGGGAAAATGATGAAGTCGCG 540
QY 1241 CTTACTGTAGAGGCTATCAAAAGTAGCGGAAGTGTCTATGATATAGCAATACACTAAGA 1300
DB 541 CTTACTGTAGAGGCTATCAAAAGTAGCGGAAGTGTCTATGATATAGCAATACACTAAGA 600
QY 1301 ATTAAGGTAACCCCTCTCTCAACTATTAATGATGACGAGCATTAATCTTTGGATAAAAAC 1360
DB 601 ATTAAGGTAACCCCTCTCTCAACTATTAATGATGACGAGCATTAATCTTTGGATAAAAAC 660
QY 1361 AAT 1363
DB 661 AAT 663

```

RESULT 9

US-08-470-953A-2
Sequence 2, Application US/08470953A
Patent No. 6346407
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
APPLICANT: ERIC DE BUYL
APPLICANT: PIERRE LEDOUX
APPLICANT: RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington

```

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..663
FEATURE:
NAME/KEY: CDS
LOCATION: 1..663
US-08-470-953A-2

```

Query Match 43.8%; Score 663; DB 3; Length 663;

Best Local Similarity 100.0%; Pred. No. 2.4e-168;

Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 701 CAAATCGTCACGACAAATCCATTGGCAACCAAGGATGCTATGATTAATGAAATTTGGAAA 760
DB 1 CAAATCGTCACGACAAATCCATTGGCAACCAAGGATGCTATGATTAATGAAATTTGGAAA 60
QY 761 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGCGCGGTACGTTCAATGCGGCAATGG 820
DB 61 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGCGCGGTACGTTCAATGCGGCAATGG 120
QY 821 AACAAATGTTAAACAAATATTTTCGTAAGGTAAAGGATTAATTAATGAAACACACAC 880
DB 121 AACAAATGTTAAACAAATATTTTCGTAAGGTAAAGGATTAATTAATGAAACACACAC 180
QY 881 CAACAAATGTTAAACAAATGTTTCGTAAGGTAAAGGATTAATTAATGAAACACACAC 940
DB 181 CAACAAATGTTAAACAAATGTTTCGTAAGGTAAAGGATTAATTAATGAAACACACAC 240
QY 941 TATTTATGCGTCTATGTTGGACTGTTGACCCCTTTGTCGAATATTAATTTGTCGACAGT 1000
DB 241 TATTTATGCGTCTATGTTGGACTGTTGACCCCTTTGTCGAATATTAATTTGTCGACAGT 300
QY 1001 TGGGGCAACTGGCGTCCACGAGGACCAAGCTTAAGGGACCATCACTGTTGATGGAGGA 1060
DB 301 TGGGGCAACTGGCGTCCACGAGGACCAAGCTTAAGGGACCATCACTGTTGATGGAGGA 360
QY 1061 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACA 1120
DB 361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACA 420
QY 1121 TTTAAACAATATTTGGAGTGTTCGAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACG 1180

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Matches 646; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 620 ATGAGCAAAAGAAATGACGTTGATTTTACGCTTTTGTGCTTGTGCTTACCTTA 679
 Db |||||
 QY 1 ATGAGCAAAAGAAATGACGTTGATTTTACGCTTTTGTGCTTGTGCTTACCTTA 60
 Db |||||
 QY 680 CTGCGAGAAATATTCAGGCAAAATCGTCACGCAAAATTCATTTGGCAACACGATGGC 739
 Db |||||
 QY 61 CTGCGAGAAATATTCAGGCAAAATCGTCACGCAAAATTCATTTGGCAACACGATGGC 120
 Db |||||
 QY 740 TATGATTTATGATTTTGGAAAGATGCGGTGCTCTGGGACAAATGATTTCTCAATCATGGC 799
 Db |||||
 QY 121 TATGATTTATGATTTTGGAAAGATGCGGTGCTCTGGGACAAATGATTTCTCAATCATGGC 180
 Db |||||
 QY 800 GGTAGTTTCAGTGCCCAATGGAACAAATGTTTACACATATTTATTCGTTAAAGGTTAAAAA 859
 Db |||||
 QY 181 GGTAGTTTCAGTGCCCAATGGAACAAATGTTTACACATATTTATTCGTTAAAGGTTAAAAA 240
 Db |||||
 QY 860 TTCAATGAAACAAACACACCAAAAGTTGGTAAACATGTCATTAACCTACGAGCCCAAC 919
 Db |||||
 QY 241 TTCAATGAAACAAACACACCAAAAGTTGGTAAACATGTCATTAACCTACGAGCCCAAC 300
 Db |||||
 QY 920 TTCCACCAAAATGGAATGCGTATTTATGCGTCTATGTTGACCTTGTGACCTTGTGTC 979
 Db |||||
 QY 301 TTCCACCAAAAGGAAATGCGTATTTATGCGTCTATGTTGACCTTGTGACCTTGTGTC 360
 Db |||||
 QY 980 GAATATTATGTCGACGATTTGGGCAACTGCGCTCCACGAGGACCAACGCTTAAGGG 1039
 Db |||||
 QY 361 GAATATTATGTCGACGATTTGGGCAACTGCGCTCCACGAGGACCAACGCTTAAGGG 420
 Db |||||
 QY 1040 ACCATCACTGTTGATGGGAAACATATGATATCTACGAGCTCTTTAGAGTCAATCAACCC 1099
 Db |||||
 QY 421 ACCATCACTGTTGATGGGAAACATATGATATCTACGAGCTCTTTAGAGTCAATCAACCC 480
 Db |||||
 QY 1100 TCCATTAAGGGATGCGCAATTTAAACAAATTTGGAGTGTTCGAAGATCGAAACGACG 1159
 Db |||||
 QY 481 TCTATTTCAGGCAACGCGCACTTCAATCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db |||||
 QY 1160 AGTGCAGATTTCTGTCAGCAACCACTTTAGAGCTGCGGAAACCTTAGGAGTGAATG 1219
 Db |||||
 QY 541 ACAGGCACTGTCACGCGCAACCACTTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 Db |||||
 QY 1220 GGGAAATGATGAAGTCTGCTTACTGTAGAGGCTATCAAGTGTAGGAGTGTCTAAT 1279
 Db |||||
 QY 601 GGTGATTTCAATTTACAGATCTGTTACTGAGGCTACCAATCTACCGGAAGTCTAAT 660
 Db |||||
 QY 1280 GTATATGCAATACATGAATTAACGTTAAACCTCTCTCACTATTAGTAAATGACGAG 1339
 Db |||||
 QY 661 GTATATGCAATACATGAATTAACGTTAAACCTCTCTCACTATTAGTAAATGACGAG 720
 Db |||||
 QY 1340 AGCATAACTTTGGATAAAAAACAAT 1363
 Db |||||
 QY 721 AGCATAACTTTAGATAAAAAACAAT 744
 Db |||||

RESULT 12
 US-08-275-526C-1
 ; Sequence 1, Application US/08275526C
 ; Patent No. 6180382
 ; GENERAL INFORMATION:
 ; APPLICANT: DE BUYL, ERIC
 ; APPLICANT: LAHAYE, ANDR E
 ; APPLICANT: LEDOUX, PIERRE
 ; APPLICANT: AMORY, ANTOINE
 ; APPLICANT: DETROZ, REN
 ; APPLICANT: VETTER, ROMAN
 ; APPLICANT: VETTER, ROMAN
 ; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
 ; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
 ; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 ; TITLE OF INVENTION: USE THEREOF
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
 STREET: 2000 K St., N.W., Suite 200
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/275,526C
 FILING DATE: 15-JUL-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gadiano, Wilhem F.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-49
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 429-0625
 TELEFAX: (202) 293-0625
 TELEX: 650 383 5605
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1022 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Bacillus pumilus
 STRAIN: PRL B12
 US-08-275-526C-1

Query Match 18.7%; Score 282.8; DB 3; Length 1022;
 Best Local Similarity 62.1%; Pred. No. 3.4e-66;
 Matches 481; Conservative 0; Mismatches 287; Indels 6; Gaps 2;

QY 599 AATTAAAGGAGGAATGCTTAATGAGACAAAGAAATGACGTTGATTTAGCTTTTAA 658
 Db |||||
 QY 165 AAAAAGGAGGAGGATGGAATGAAATTTGAAAGATTTAGGCTGTTGTTGATGTGT 224
 Db |||||
 QY 659 GTTTGTTTTCACATACTTACCTGCAAAATTAATTCAGGCACAAATCGTCACGCAAT 718
 Db |||||
 QY 225 ATTGATTTGCTGACACCTGACGCTGTCGCGCTCATCGGAAACGATTTATGATAT 284
 Db |||||
 QY 719 TCCATTGCGCAACCACTGCTATGATTTGAAATTTTGGAAAGATAGCGGTGCTCTGG 778
 Db |||||
 QY 285 AGGATAGGACACACGCGGATACGATTTTGAATTTATGGAAGGATTAC---GGAATACC 341
 Db |||||
 QY 779 ACATGATTTCAATCATGCGGTGACGTTGAGTCCCAATGGAACATGTTAAACATA 838
 Db |||||
 QY 342 TCGATGACCTCAATAACGCGGGGCAATTTAGTCAAGCTGGAACAAATTTGGAATGCC 401
 Db |||||
 QY 839 TTATTCGTAAGGTAAGAAATTCATGAAACACAAACACCAAGTTGGTAAACATG 898
 Db |||||
 QY 402 TTATTCGAAAGGAAAGAGTTGATTCCTAAACTCATCATCACTTTGGCAACATC 461
 Db |||||
 QY 899 TCCATAAACTACGAGGCAACTTCCAAACCAATTTGTAATCGTATTTATCGCTTATGGT 958
 Db |||||
 QY 462 TCCATCAACTACACGCGCTTTAAACCGCGGGGAAATTCCTATTATTTATGCTATGGC 521
 Db |||||
 QY 959 TGGACTGTCACCTCTTGTGCAATATATATTTGTGACAGTTGGGCAACTGCGCTCCA 1018
 Db |||||
 QY 522 TGGACAAATCTCCATTAGCTGAATACATATTGTTGAGTCATGGGGCAATATCGCTCCA 581
 Db |||||
 QY 1019 CCAGGACCAACGCTTAAGGGGACCATCACTGTTGATGGAGGAAACATATGATATCTACGAG 1078
 Db |||||
 QY 582 ACAGG---ACGTATAAGGATCAATTTATGCCGATGAGGACATATGACATATAGAA 638
 Db |||||
 QY 1079 ACTCTTAGAGTCAATCAACCTCCATTAAGGGATTCGCCACATTTAAACAAATATGAGT 1138
 Db |||||

Db 639 ACGCTCCGTGCTCAATCAGCCTTCTATCATTTGGAGAGCTACCTTCAAAACAATTTGGAGT 698
 QY 1139 GTTCGAAGATCGAAGCGACGAGTGTGTCAGCAACCACTTTAGACGGTGG 1198
 Db 699 GTACGTCAAAACAAACGCAACAGCGGACGGTCTCCGTGAGTGAGCAATTTAAAAAATGG 758
 QY 1199 GAAAACTTAGGATGAATATGCGGAAATGTAAGTCGCTTACTGTAGAGGCTAT 1258
 Db 759 GAAAGCTTAGGATGCAATGCGAATGGAAATGTAAGCAACAGCAATTAAGTGAAGGCTAC 818
 QY 1259 CAAAGTAGCGGAGTCTAATGATATAGCAATACACTAAGAAATTAACGGTAAACCTCTC 1318
 Db 819 CGAAGCAACGGAAGTGGGAATGTCATGACGAATCAGCTGATTCGATAAAAGCATATG 878
 QY 1319 TCAACTATTAGTAAGCAGAGCATACTTTGGATAAAACAATTAATAATCC 1372
 Db 879 AAAAAAGCCAGCAAAAAATGGCTGCTTTTCTATGATAATTTTCAACTTCC 932

RESULT 13

US-08-275-526C-35
 ; Sequence 35, Application US/08275526C
 ; Patent No. 6180382
 ; GENERAL INFORMATION:
 ; APPLICANT: DE BUYL, ERIC
 ; APPLICANT: LAHAYE, ANDR E
 ; APPLICANT: LEDOUX, PIERRE
 ; APPLICANT: AMORY, ANTOINE
 ; APPLICANT: DETROZ, REN
 ; APPLICANT: ANDRE, CHRISTOPHE
 ; APPLICANT: VETTER, ROMAN
 ; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
 ; TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
 ; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 ; TITLE OF INVENTION: USE THEREOF
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
 ; STREET: 2000 K St., N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/275,526C
 ; FILING DATE: 15-JUL-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gadiano, Wilhem F.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-49
 ; TELEPHONE: (202) 429-0625
 ; TELEFAX: (202) 293-0625
 ; TELEX: 650 383 5605
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1022 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: genomic DNA
 ; US-08-275-526C-35

Query Match 18.7%; Score 282.8; DB 3; Length 1022;
 Best Local Similarity 62.1%; Pred. No. 3.4e-66;
 Matches 481; Conservative 0; Mismatches 287; Indels 6; Gaps 2;

QY 599 AATTAAGAGGAGGAGTGCCTAATGAGACAAAGAAATTTAGCTTTTATTTAGCCCTTTTAA 658
 Db 165 AAAAAAGGAGGAGGATGGAATGAAATTTGAAAGATTGAGCTGTTGTTGTGATGTGT 224
 QY 659 GTTTGTTTGGTCACTAACTTACCTGCGGAAATTAATTTAGGACACAATCGTCAACCAAT 718
 Db 225 ATTGATTTGCTGACACTGACGCTGTCGCGGCTCATGGGAAACGAATTTATGATATAT 284
 QY 719 TCCATTGCAACACGATGGCTATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGG 778
 Db 285 AGGATAGGGAACACACGCGGATACGAATTTGAATTTATGAGGATTAC---GGAATACC 341
 QY 779 ACAATGATTTCAATCATGCGGTAAGTTCAGTGCCTTCAATGGAACAATTTGTAACACATA 838
 Db 342 TCGATGACACTCAATAACGCGGGGCAATTTAGTGAAGCTGGAACAATTTGGAATGCC 401
 QY 839 TTATTCGTAAGGTAAAAATTTCAATGAAACACAAACACACCAACAAGTTGGTAACATG 898
 Db 402 TTATTTGAAAGGAAGAAGTTTGAATTTCCACTAAACCTCATCATCAACTTGGCAATC 461
 QY 899 TCCATAAACTACGGAGCCAACTTCCAAACCAATGTAATGCGTATTTATGCGTCTATGTT 958
 Db 462 TCCATCAACTACACGAGCCCTTTAAACCGGGCGGAATTCCTATTTATGTTCTATGGC 521
 QY 959 TGGACTGTTGACCCCTTTGTGCAATTTATATTGTCGACAGTTGGGGCAACTGGGGTCCA 1018
 Db 522 TGGACACAATCTCCATTAGCTGAATACATTTGTTGAGTCATGCGGCACATATCGTCCA 581
 QY 1019 CCAGGAGCAACGCTTAAGGGACCACTCACTGTTGATGAGGAGCAATATGATATCTACGAG 1078
 Db 582 ACAGG---AACGTATAAAGGATCATTTTATGCCGATGGAGGCACATATGACATATATGAA 638
 QY 1079 ACTCTTAGAGTCAATCAACCCCTCCATTAAGGGGATTTGCCACATTTAAACAATTTGGAGT 1138
 Db 639 ACGCTCCGTGCAATCAGCCTTCTATCATTTGAGAGCGTACCTTCAACCAATTTGGAGT 698
 QY 1139 GTTCGAAGATCGAAACGACAGTGGCAGCATTTCTGTGACAAACCACTTTAGAGCGTGG 1198
 Db 699 GTACGTCAAACAAACGACAGCGGACGGTCTCCGTGAGTGAGCATTTTAAAAAATGG 758
 QY 1199 GAAAACTTAGGATGAATATGGGAAAAATGTAAGTCGCGCTTACTGTAGAGGCTAT 1258
 Db 759 GAAAGCTTAGGATGCCAATGGGAAAAATGTAAGAAACAGCAATTAACCTGAGAGGCTAC 818
 QY 1259 CAAAGTAGCGGAGTGAATGTAATGATATAGCAATACACTAAGAAATTAACGTAACCCCTCTC 1318
 Db 819 CGAAGCAACGGAAGTGGGAATGTCATGACGAATCAGCTGATTCGATAAAAGCATATG 878
 QY 1319 TCAACTATTAGTAATGACGAGAGCATACTTTGGATAAAACAATTTAAAAATCC 1372
 Db 879 AAAAAAGCCAGCAAAAAATGGCTGCTTTTCTATGATAATTTTCAACTTCC 932

RESULT 14

US-09-076-677-1
 ; Sequence 1, Application US/09076677
 ; Patent No. 6423523
 ; GENERAL INFORMATION:

APPLICANT: DE BUYL, ERIC
 LAHAYE, ANDR E
 LEDOUX, PIERRE
 AMORY, ANTOINE
 DETROZ, RENE
 ANDRE, CHRISTOPHE
 VETTER, ROMAN

TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
 EXPRESSION VECTORS FOR SUCH XYLANASE AND
 OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 USE THEREOF

NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
 STREET: 2000 K St., N.W., Suite 200

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEX: 650 383 5605
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORGANISM: Bacillus pumilus
STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-076-677-1

Query Match 18.7%; Score 282.8; DB 4; Length 1022;
Best Local Similarity 62.1%; Pred. No. 3.4e-66;
Matches 481; Conservative 0; Mismatches 28; Indels 6; Gaps 2;

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DB 225 ATTGATTTGTGCTGACACTGACGCTGTCCGCTCATGCGGAAACGATTTATGATAAT 284
QY 719 TCCATTGGCAACACGATGGCTATGATTATGAATTTTGAAGATAGCGGTGGCTCTGGG 778
DB 285 AGGATAGGACACACAGCGGATACGATTTGAATTTAGAGGATTAC---GGAAATACC 341
QY 779 ACAATGATTCTCAATCATGGGGTACGTTAGTGCCCAATGGAACAAATGTTAAACAACATA 838
DB 342 TCGATGACACTCAATAACGGGGGCACTTTAGTGAAGCTGGAACAAATTTGGAAATGCC 401
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RESULT 15
US-09-076-677-35
Sequence 35, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
LAHAYE, ANDREE
LEDOUX, PIERRE
AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-09-076-677-35

Query Match		18.7%	Score 282.8;	DB 4;	Length 1022;
Best Local Similarity		62.11%;	Pred. No. 3.4e-66;		
Matches 481;		Conservative 0;	Mismatches 287;	Indels 6;	Gaps 2;
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Search completed: November 11, 2004, 01:34:23
Job time : 176.81 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 21:26:43 ; Search time 967.351 Seconds
(without alignments)
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Perfect score: 1513
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues
Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	744	49.2	744	9	US-09-909-207-4
4	744	49.2	744	9	US-09-909-207-5
5	663	43.8	663	9	US-09-909-207-1
6	663	43.8	663	9	US-09-909-207-2
7	619	40.9	619	9	US-09-909-207-12
8	150	9.9	150	9	US-09-909-207-13
9	119.4	7.9	1375	9	US-09-770-621-1
10	119.4	7.9	1375	15	US-10-286-993-1
11	115.2	7.6	596	15	US-10-307-441-39
12	111.4	7.4	942	14	US-10-213-990-71
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					Sequence 4, Appl
					Sequence 5, Appl
					Sequence 1, Appl
					Sequence 2, Appl
					Sequence 12, Appl
					Sequence 13, Appl
					Sequence 1, Appl
					Sequence 39, Appl
					Sequence 71, Appl

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15	106	7.0	2898	15	US-10-299-393-1	Sequence 1, Appl
16	104.8	6.9	712	14	US-10-213-990-64	Sequence 64, Appl
17	103.6	6.8	666	14	US-10-213-990-65	Sequence 65, Appl
18	96.8	6.4	739	14	US-10-213-990-67	Sequence 67, Appl
19	86.8	5.7	678	10	US-09-803-454-3	Sequence 3, Appl
20	84.2	5.6	1027	16	US-10-244-596-6	Sequence 6, Appl
21	84	5.6	1027	16	US-10-244-596-2	Sequence 2, Appl
22	83.2	5.5	645	15	US-10-237-386-10	Sequence 10, Appl
23	83.2	5.5	657	15	US-10-237-386-11	Sequence 11, Appl
24	82.6	5.5	1011	16	US-10-244-596-11	Sequence 11, Appl
25	82.6	5.5	1011	16	US-10-244-596-12	Sequence 12, Appl
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27	82.6	5.5	1023	16	US-10-244-596-5	Sequence 5, Appl
28	82.6	5.5	1023	16	US-10-244-596-7	Sequence 7, Appl
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34	81	5.4	1023	16	US-10-244-596-10	Sequence 10, Appl
35	79.4	5.2	1023	16	US-10-244-596-4	Sequence 4, Appl
36	79	5.2	2225	10	US-03-750-070A-8	Sequence 8, Appl
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38	77.2	5.1	749	18	US-10-425-115-82922	Sequence 82922, A
39	75.8	5.0	818	18	US-10-425-115-37173	Sequence 37173, A
40	73.8	4.9	850	18	US-10-425-115-177283	Sequence 177283, A
41	72.4	4.8	588	15	US-10-237-386-9	Sequence 9, Appl
42	72.4	4.8	983	9	US-09-467-368-1	Sequence 1, Appl
43	57.6	3.8	3673778	15	US-10-312-841-2	Sequence 2, Appl
44	55.8	3.7	3673778	15	US-10-312-841-1	Sequence 1, Appl
45	54.2	3.6	2054	15	US-10-419-969-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-909-207-10
; Sequence 10, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUIJL
; PIERRE LEDOUX
; RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSER: WILLIAM BRINKS HOFER GILSON & LJONE

STREET: 2000 K St., N.W., Suite 200

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/909,207

APPLICATION NUMBER: US/09/909,207

FILING DATE: 19-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/470,953

FILING DATE: 06-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Wilhem F. Gadiano, Esq.

REGISTRATION NUMBER: 37,136

```

; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1513 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
;
US-09-909-207-10

Query Match 100.0%; Score 1513; DB 9; Length 1513;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 11, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
;
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: 620..1363
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 701..1363
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 620..700
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-909-207-11

Query Match 100.0%; Score 1513; DB 9; Length 1513;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGAATTGTATATCTAATGATTAACGACAAATCGTCACCTGTTTAACTATCTC 60
Db 1 AAATTGAATTGTATATCTAATGATTAACGACAAATCGTCACCTGTTTAACTATCTC 60

Qy 61 AAACCAATCTCTTTTAACTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 120
Db 61 AAACCAATCTCTTTTAACTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 120

Qy 121 ATAGGAATCTTTCCCAATTTGCAAGACGATAAAAAATCTTTTCCCAATTTTATCTATCG 180
Db 121 ATAGGAATCTTTCCCAATTTGCAAGACGATAAAAAATCTTTTCCCAATTTTATCTATCG 180

Qy 181 CTTTGATCGGTTAAATTTGTAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTT 240
Db 181 CTTTGATCGGTTAAATTTGTAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTT 240

Qy 241 CATTAAATCACAGTTAAACGCTAGAGTCATCTTTTCCGTTCTCAAAAATACCTGAAGAAC 300
Db 241 CATTAAATCACAGTTAAACGCTAGAGTCATCTTTTCCGTTCTCAAAAATACCTGAAGAAC 300

Qy 301 ATTTATGTCATATTTTCTCAGCGGCTCCATAATGGAATATATATATCTTTTATACATA 360
Db 301 ATTTATGTCATATTTTCTCAGCGGCTCCATAATGGAATATATATATCTTTTATACATA 360

Qy 361 TTAAGTAAATTTAGTATATCTTGGGTTATCAAAATGTGAGATATCTAAATTTGATCAAA 420
Db 361 TTAAGTAAATTTAGTATATCTTGGGTTATCAAAATGTGAGATATCTAAATTTGATCAAA 420

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Qy 421 AGCAGCTATCCAAAAAACACATGATGTTGACCTCTTTAAAGAAAGTGTCACCTATCTATGAAA 480
Db 421 AGCAGCTATCCAAAAAACACATGATGTTGACCTCTTTAAAGAAAGTGTCACCTATCTATGAAA 480

Qy 481 GATAATTTATCCAGTTTCAAAATTTGAATAGTGTGTATGGAATAGTGTGAAATGTCACATG 540
Db 481 GATAATTTATCCAGTTTCAAAATTTGAATAGTGTGTATGGAATAGTGTGAAATGTCACATG 540

Qy 541 CTGTGAAAGGAGGGTAGGTAGTACCGTAGACTTCAATTACCAAAAATTTAGTTGTAAAAAAA 600
Db 541 CTGTGAAAGGAGGGTAGGTAGTACCGTAGACTTCAATTACCAAAAATTTAGTTGTAAAAAAA 600

Qy 601 TTAAGAGGAGGAATGCCCTAATAGAGCAAAAAGAAATTTAGCTTTAGCTTTTATGCTTTT 660
Db 601 TTAAGAGGAGGAATGCCCTAATAGAGCAAAAAGAAATTTAGCTTTAGCTTTTATGCTTTT 660

Qy 661 TTGTTTTCGACTTAACCTTACCTGCGAGAAATTAATTCAGGCACAAATTCGTCACCGACATTC 720
Db 661 TTGTTTTCGACTTAACCTTACCTGCGAGAAATTAATTCAGGCACAAATTCGTCACCGACATTC 720

Qy 721 CATTGGCAACCAACGATGGCTATGATTATCAATTTTGGAAAGATAGCGGTGGCTCTGGGAC 780
Db 721 CATTGGCAACCAACGATGGCTATGATTATCAATTTTGGAAAGATAGCGGTGGCTCTGGGAC 780

Qy 781 AATGATTTCTCAATCATGCGGTACGTTCAAGTCCCAATGGAACAATTTGGAACAATATT 840
Db 781 AATGATTTCTCAATCATGCGGTACGTTCAAGTCCCAATGGAACAATTTGGAACAATATT 840

Qy 841 ATTCGTTAAAGSTAAAAAATTTCAATGAAACACAAACACCAACCAAGTTGGTAAACATGTC 900
Db 841 ATTCGTTAAAGSTAAAAAATTTCAATGAAACACAAACACCAACCAAGTTGGTAAACATGTC 900

Qy 901 CATAAATACGAGGACCACTTCCAAACCAATGGTAAATGGTAAATTTATGCGTCTATGGTTG 960
Db 901 CATAAATACGAGGACCACTTCCAAACCAATGGTAAATGGTAAATTTATGCGTCTATGGTTG 960

Qy 961 GACTGTTGACCTCTTGTGCAATATTAATTCGACAGTTCGGGCAATCGCGTCCACC 1020
Db 961 GACTGTTGACCTCTTGTGCAATATTAATTCGACAGTTCGGGCAATCGCGTCCACC 1020

Qy 1021 AGGAGCAACGCTTAAGGGACCATCACTGTTGATGGAGAAACATATGATATCTACGAGAC 1080
Db 1021 AGGAGCAACGCTTAAGGGACCATCACTGTTGATGGAGAAACATATGATATCTACGAGAC 1080

Qy 1081 TCTTAGAGTCAATCAACCTCCATTAAGGGGATGCGCAATTTAAACAATATTGGAGTGT 1140
Db 1081 TCTTAGAGTCAATCAACCTCCATTAAGGGGATGCGCAATTTAAACAATATTGGAGTGT 1140

Qy 1141 TCGAAGATCGAAACGACGAGTGGACGATTTCTGTACGAAACCACTTTAGAGCGTGGGA 1200
Db 1141 TCGAAGATCGAAACGACGAGTGGACGATTTCTGTACGAAACCACTTTAGAGCGTGGGA 1200

Qy 1201 AAACCTTAGGATGAATATGGGGAATATGTAAGTTCGCGCTTACTGTAGAGGCTATCA 1260
Db 1201 AAACCTTAGGATGAATATGGGGAATATGTAAGTTCGCGCTTACTGTAGAGGCTATCA 1260

Qy 1261 AAGTACGGAAGTGTAAATGTTATATAGCAATACACTAAGAAATTAACGCTTAACCTCTCTC 1320
Db 1261 AAGTACGGAAGTGTAAATGTTATATAGCAATACACTAAGAAATTAACGCTTAACCTCTCTC 1320

Qy 1321 AACTATTAGTAATGACGAGACGATAACTTTTGGATAAAAACAATTTAAATAATCTTTATCTCT 1380
Db 1321 AACTATTAGTAATGACGAGACGATAACTTTTGGATAAAAACAATTTAAATAATCTTTATCTCT 1380

Qy 1381 TTGGTTTCAAGTTCTCAATTTTCAATAACCTCCGGTTGGATCTTTTCCACACGGGAGG 1440
Db 1381 TTGGTTTCAAGTTCTCAATTTTCAATAACCTCCGGTTGGATCTTTTCCACACGGGAGG 1440

Qy 1441 TTTTATTGGAAGGTTAAAGTATAGTATCTCCGATTTCCATCCAGAGGAATGCTTTGAAACA 1500
Db 1441 TTTTATTGGAAGGTTAAAGTATAGTATCTCCGATTTCCATCCAGAGGAATGCTTTGAAACA 1500

Qy 1501 CCTCCGTCACCTAG 1513

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Db      1501 CCTCGTCACTAG 1513
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Db      1501 CCTCGTCACTAG 1513
|||||
RESULT 3
US-09-909-207-4
; Sequence 4, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
;           ERIC DE BOYL
;           PIERRE LEDOUX
;           RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
;                   DNA molecule, processes for preparation of this xylanase
;                   and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-909-207-4
Query Match          49.2%; Score 744; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.3e-166;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      620 ATGACACAAAGAAATGACGTTGATTTAGCCTTTTGTGTTGTTGCTACTAACCTTA 679
Db      1 ATGACACAAAGAAATGACGTTGATTTAGCCTTTTGTGTTGTTGCTACTAACCTTA 60
QY      680 CCTGCAGAAATATTCAGGCAAAATCGTCACCGCAATTCATTTGGCAACACGATGC 739
Db      61 CCTGCAGAAATATTCAGGCAAAATCGTCACCGCAATTCATTTGGCAACACGATGC 120
QY      740 TATGATTATGATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCTCAATCATGGC 799
Db      121 TATGATTATGATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCTCAATCATGGC 180
QY      800 GGTACGTTCACTGCGCCCAATGGAAACAATGTTTAAACAACATATTATTCCTCGTAAAGGTA 859

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Db      181 GGTACGTTCACTGCGCCCAATGGAAACAATGTTTAAACAACATATTATTCCTGTAAGGTAA 240
QY      860 TTCAATGAAACACAAACACACACCAACCAAGTTGGTGAACATATGTCATAAATCTACGAGCC 919
Db      241 TTCAATGAAACACAAACACACACCAACCAAGTTGGTGAACATATGTCATAAATCTACGAGCC 300
QY      920 TTCCAAACCAATGTTGATGCGTATTTATGCTGCTATGTTGGAGTGTGACCTCTTGTC 979
Db      301 TTCCAAACCAATGTTGATGCGTATTTATGCTGCTATGTTGGAGTGTGACCTCTTGTC 360
QY      980 GAATATTATATTTGTCGACAGTTGGGGCAACTGGCGTCCACCAGAGCAACGCCCTAAGGGG 1039
Db      361 GAATATTATATTTGTCGACAGTTGGGGCAACTGGCGTCCACCAGAGCAACGCCCTAAGGGG 420
QY      1040 ACCATCACTGTTGATGAGGAAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 1099
Db      421 ACCATCACTGTTGATGAGGAAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCC 480
QY      1100 TCCATTAAAGGGATTGCCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACG 1159
Db      481 TCCATTAAAGGGATTGCCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGACG 540
QY      1160 AGTGGCAGATTTCTGTGTCAGCAACCACTTTAGAGCGTGGGAAACTTTAGGATGAATATG 1219
Db      541 AGTGGCAGATTTCTGTGTCAGCAACCACTTTAGAGCGTGGGAAACTTTAGGATGAATATG 600
QY      1220 GGGAAATGATGAAATCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAGTGTCTAAT 1279
Db      601 GGGAAATGATGAAATCGCGCTTACTGTAGAGGCTATCAAGTAGCGGAGTGTCTAAT 660
QY      1280 GTATATAGCAATACACTAAGAAATTAACGTAACCCCTCTCTCAACTATTAGTAATGACGAG 1339
Db      661 GTATATAGCAATACACTAAGAAATTAACGTAACCCCTCTCTCAACTATTAGTAATGACGAG 720
QY      1340 AGCAATACTTTGGATAAAACAAT 1363
Db      721 AGCAATACTTTGGATAAAACAAT 744
RESULT 4
US-09-909-207-5
; Sequence 5, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
;           ERIC DE BOYL
;           PIERRE LEDOUX
;           RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
;                   DNA molecule, processes for preparation of this xylanase
;                   and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Bacillus
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-909-207-4
Query Match          49.2%; Score 744; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 1.3e-166;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      620 ATGACACAAAGAAATGACGTTGATTTAGCCTTTTGTGTTGTTGCTACTAACCTTA 679
Db      1 ATGACACAAAGAAATGACGTTGATTTAGCCTTTTGTGTTGTTGCTACTAACCTTA 60
QY      680 CCTGCAGAAATATTCAGGCAAAATCGTCACCGCAATTCATTTGGCAACACGATGC 739
Db      61 CCTGCAGAAATATTCAGGCAAAATCGTCACCGCAATTCATTTGGCAACACGATGC 120
QY      740 TATGATTATGATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCTCAATCATGGC 799
Db      121 TATGATTATGATTTTGGAAAGATAGCGTGGCTCTGGGACAAATGATTTCTCAATCATGGC 180
QY      800 GGTACGTTCACTGCGCCCAATGGAAACAATGTTTAAACAACATATTATTCCTCGTAAAGGTA 859

```

NAME: Wilhem F. Gadiano, Esq.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-40
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-429-0625
 TELEFAX: (202) 293-1850
 TELEX: 650 383-5605
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 744 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 STRAIN: Bacillus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..744
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 82..744
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 1..81
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-909-207-5
 Query Match 49.2%; Score 744; DB 9; Length 744;
 Best Local Similarity 100.0%; Pred. No. 1.3e-166;
 Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 620 ATGAGACAAAGAAATGACGTTGATTTAGCTTTTATGCTTTTATGTTGTTGCTACCTTA 679
 Db 1 ATGAGACAAAGAAATGACGTTGATTTAGCTTTTATGCTTTTATGTTGTTGCTACCTTA 60
 QY 680 CTGCGAGAATAATTCAGGCACAAATCGTCACGCAATTCATTCGACCAACACGATGC 739
 Db 61 CTGCGAGAATAATTCAGGCACAAATCGTCACGCAATTCATTCGACCAACACGATGC 120
 QY 740 TATGATTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACCAATGATTTCTCAATCATGCG 799
 Db 121 TATGATTATGAATTTTGGAAAGATAGCGTGGCTCTGGGACCAATGATTTCTCAATCATGCG 180
 QY 800 GGTACGTTACGTCGCCCAATGGAACAATGTTTAAACAATATATTCGTTAAAGTAAAAA 859
 Db 181 GGTACGTTACGTCGCCCAATGGAACAATGTTTAAACAATATATTCGTTAAAGTAAAAA 240
 QY 860 TTCATGAACACAAACACACCAACCAAGTTGGTAAACATGTCCTCAATCAACGAGCAAC 919
 Db 241 TTCATGAACACAAACACACCAACCAAGTTGGTAAACATGTCCTCAATCAACGAGCAAC 300
 QY 920 TTCACCAACCAATGTTATGCTGTTATGCTGTTATGCTGTTGAGTGTGACCTCTTGTG 979
 Db 301 TTCACCAACCAATGTTATGCTGTTATGCTGTTATGCTGTTGAGTGTGACCTCTTGTG 360
 QY 980 GAATATTATATTGTCGACGTTGGGCAACTGGCGTCCACGAGCAACGCTTAAGGGG 1039
 Db 361 GAATATTATATTGTCGACGTTGGGCAACTGGCGTCCACGAGCAACGCTTAAGGGG 420
 QY 1040 ACATCATCTGTTGATGAGGAACAATATGATATCTACGAGACTCTTAGAGTCAATCAACC 1099
 Db 421 ACATCATCTGTTGATGAGGAACAATATGATATCTACGAGACTCTTAGAGTCAATCAACC 480
 QY 1100 TCCATTAAGGGGATTCGCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG 1159
 Db 481 TCCATTAAGGGGATTCGCACATTTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG 540
 QY 1160 AGTGGCAGGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAATTAGGATGAATATG 1219
 Db 541 AGTGGCAGGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAATTAGGATGAATATG 600
 QY 1220 GGGAAATATGTAAGTGGCGCTTACTGTAGAGGCTATCAAGTAGCGGAAAGTCTAAT 1279

Db 601 GGGAAATATGTAAGTGGCGCTTACTGTAGAGGCTATCAAGTAGCGGAAAGTCTAAT 660
 QY 1280 GTATATAGCAATACACTAAGAAATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAG 1339
 Db 661 GTATATAGCAATACACTAAGAAATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAG 720
 QY 1340 AGCATAACTTTGGATAAAACAAT 1363
 Db 721 AGCATAACTTTGGATAAAACAAT 744
 RESULT 5
 US-09-909-207-1
 ; Sequence 1, Application US/09909207
 ; Patent No. US20020115181A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDREE LAHAYE
 ; ERIC DE BUYL
 ; PIERRE LEDOUX
 ; RENE DETROZ
 ; TITLE OF INVENTION: Xylanase, microorganisms produced it,
 ; DNA molecule, processes for preparation of this xylanase
 ; and uses thereof
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
 ; STREET: 2000 K St., N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/909,207
 ; FILING DATE: 19-Jul-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/470,953
 ; FILING DATE: 06-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilhem F. Gadiano, Esq.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-40
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-429-0625
 ; TELEFAX: (202) 293-1850
 ; TELEX: 650 383-5605
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 663 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; STRAIN: Bacillus
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 ; US-09-909-207-1
 Query Match 43.8%; Score 663; DB 9; Length 663;
 Best Local Similarity 100.0%; Pred. No. 2.3e-147;
 Matches: 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 701 CAAATCGTCCACCAATTCCTTGGCAACCAACGATGGCTATGATTATGATTTTGGAAA 760
 Db 1 CAAATCGTCCACCAATTCCTTGGCAACCAACGATGGCTATGATTATGATTTTGGAAA 60
 QY 761 GATAGCGGTGGCTCTGGGACCAATGATTTCTCAATCATGGCGGTACGTTAGTCCCAATG 820

QY 1301 ATTAACGGTAACCTCTCACTATTAGTAATGACGAGACATACCTTTGGATAAAAAC 1360
DB 601 ATTAACGGTAACCTCTCTCACTATTAGTAATGACGAGACATACCTTTGGATAAAAAC 660
QY 1361 AAT 1363
DB 661 AAT 663

RESULT 7
US-09-909-207-12
; Sequence 12, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAN BRINKS HOPER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,207
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 231-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 619 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-909-207-12

Query Match 40.9%; Score 619; DB 9; Length 619;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGAATTCGTATCTCAATGATACGACAAATCGTCACCTGTTTTAACTAACTC 60
DB 1 AAATTGAATTCGTATCTCAATGATACGACAAATCGTCACCTGTTTTAACTAACTC 60
QY 61 AAACCAATACCTCTTTATTTAACTGACCACTGTCATCTTATACAGAACATCTTT 120
DB 61 AAACCAATACCTCTTTATTTAACTGACCACTGTCATCTTATACAGAACATCTTT 120
QY 121 ATAGAACTTCCCACTTGGCAGACGATAAAATCTTTCCCTATTTTATCTATCG 180

DB 121 ATAGAACTTCCCACTTGGCAGACGATAAAATCTTTTCCCTATTTTATCTATCG 180
QY 181 CCTTGATCGGTTTAATTTGTAACCTTTTATTTTAGTTTACGTGATGTTCCCTCATTCATAC 240
DB 181 CCTTGATCGGTTTAATTTGTAACCTTTTATTTTAGTTTACGTGATGTTCCCTCATTCATAC 240
QY 241 CATTAAATCACAGTTTAAACGCTAGAGTCATCTTTTTCGGTTCCTCAAAAATACCTGAAGAAC 300
DB 241 CATTAAATCACAGTTTAAACGCTAGAGTCATCTTTTTCGGTTCCTCAAAAATACCTGAAGAAC 300
QY 301 ATTTATGTCATATTTTCTCAGCCGCTCCATAATGGAATATATATCTCTTTTATACATA 360
DB 301 ATTTATGTCATATTTTCTCAGCCGCTCCATAATGGAATATATATCTCTTTTATACATA 360
QY 361 TTAAGTAAATTAGTATATATCTTGCCTTATCAAAATGTGAGATAATCTTAATGATCAAAACA 420
DB 361 TTAAGTAAATTAGTATATATCTTGCCTTATCAAAATGTGAGATAATCTTAATGATCAAAACA 420
QY 421 AGCAGCTATCCAAAAACACATGATGTTGACCTCTTAAAGAGAGTGCATCTATCTATGAAAA 480
DB 421 AGCAGCTATCCAAAAACACATGATGTTGACCTCTTAAAGAGAGTGCATCTATCTATGAAAA 480
QY 481 GATAATTTATCCAGTTTCAAAAATTTGAAATAGTGTGATGGAATAGTTTGAATGTCAACTG 540
DB 481 GATAATTTATCCAGTTTCAAAAATTTGAAATAGTGTGATGGAATAGTTTGAATGTCAACTG 540
QY 541 CTGTGAAAGGAGGTAGGTAGTACCGTAGCTTCACTTACCAAAAAATTTAGTTGTAAAAAAA 600
DB 541 CTGTGAAAGGAGGTAGGTAGTACCGTAGCTTCACTTACCAAAAAATTTAGTTGTAAAAAAA 600
QY 601 TTAAGAGGAGGAATGCCTA 619
DB 601 TTAAGAGGAGGAATGCCTA 619

RESULT 8
US-09-909-207-13
; Sequence 13, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
; ERIC DE BUYL
; PIERRE LEDOUX
; RENE DETROZ
; TITLE OF INVENTION: Xylanase, microorganisms produced it,
; DNA molecule, processes for preparation of this xylanase
; and uses thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAN BRINKS HOPER GILSON & LIONE
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,207
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,953
; FILING DATE: 06-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-0625
; TELEFAX: (202) 231-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 619 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-909-207-12

Query Match 40.9%; Score 619; DB 9; Length 619;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGAATTCGTATCTCAATGATACGACAAATCGTCACCTGTTTTAACTAACTC 60
DB 1 AAATTGAATTCGTATCTCAATGATACGACAAATCGTCACCTGTTTTAACTAACTC 60
QY 61 AAACCAATACCTCTTTATTTAACTGACCACTGTCATCTTATACAGAACATCTTT 120
DB 61 AAACCAATACCTCTTTATTTAACTGACCACTGTCATCTTATACAGAACATCTTT 120
QY 121 ATAGAACTTCCCACTTGGCAGACGATAAAATCTTTCCCTATTTTATCTATCG 180

```

;
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-909-207-13

Query Match          9.9%; Score 150; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.3e-25;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1364 TAAATAATCCTTATCTCTTTCGGTTCAGTTCCTATTATTTTCAATAAACCCTCCCGGTTGGA 1423
Db 1 TAAATAATCCTTATCTCTTTCGGTTCAGTTCCTATTATTTTCAATAAACCCTCCCGGTTGGA 60

QY 1424 TCTTTTCCAAACGGGAGGTTTATTTCGAAAGGTTAAGTATAGTATATCTCGATTCCATCCA 1483
Db 61 TCTTTTCCAAACGGGAGGTTTATTTCGAAAGGTTAAGTATAGTATATCTCGATTCCATCCA 120

QY 1484 GAGGAATGCTTGAACACCTCCGTCACCTAG 1513
Db 121 GAGGAATGCTTGAACACCTCCGTCACCTAG 150

RESULT 9
US-09-770-621-1
; Sequence 1, Application US/09770621
; Patent No. US20010024815A1
; GENERAL INFORMATION:
; APPLICANT: M ntyl , Arja
; APPLICANT: Vehmaanpera, Jari
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lahtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,621
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/590,563
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.

;
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 1050.0340003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: No. US20010024815A1 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 303..1334
US-09-770-621-1

Query Match          7.9%; Score 119.4; DB 9; Length 1375;
Best Local Similarity 57.1%; Pred. No. 7.1e-18;
Matches 238; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 898 GTCCATAAACTACGGAGCCAACTTCCAAACCAATGGTAATCGGTATTTATCGGTCTATGG 957
Db 608 GACCGTGACCTTACAAAGCGCTCCTTCAACCCCGTGGGTAAACGGCTACCTCAGGCTCTACGG 667

QY 958 TTGGACTGTTGACCCCTCTTTCGTAATATATATTCGACAGTTTGGGCAACTGGCGTCC 1017
Db 668 CTGGACCAAGAACCCGCTCGTGCAGTACTATCATCGTCGAGAGCTGGGGCACCCTACCGGCC 727

QY 1018 ACCAGGAGCAACGCTTAAGGGGACCATCCTGTTGATGGAGGAACATATGATATCTACGA 1077
Db 728 CACCGG---CACCTACAGGGCACCGTCACCGGCGGGAACGTACGACATCTACGA 784

QY 1078 GACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAG 1137
Db 785 GACCTGGCGGTACAAACGCGCGTCCATCGAGGGCACCCGCGACCTTCCAGCAGTTCTGGAG 844

QY 1138 TGTTTCAAGATCGAAACGACAGTGGCAGCATTTCTGTACAGCAACCACTTTAGAGCGTG 1197
Db 845 GTCCGGCAGCAGAAAGCGGACCGGACCATCACCATCGGCAACCACTTCGACGCGCTG 904

QY 1198 GGAATAACTTAGGATGAATATATGGGAAATATGAAAGTCGCGCTTACTGTAGAGGCTA 1257
Db 905 GGGCCGCGCGCATGAACCTGGCGCAGCAGCTACCGAGATCATGGCGACCGAGGGGCTA 964

QY 1258 TCAAGTAGCGGAAGTGTCTATGTATATAGCAATACACTAAGATTAACGTAACCC 1314
Db 965 CCAGAGCAGCGGTAGTCCACCGTCTCCATCAGCGAGGGTGGCAACCCCGCAACCC 1021

RESULT 10
US-10-286-993-1
; Sequence 1, Application US/10286993
; Publication No. US20030148453A1
; GENERAL INFORMATION:
; APPLICANT: Mantyla, Arja
; APPLICANT: Paloheimo, Marja
; APPLICANT: Lantto, Raija
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Vehmaanpera, Jari
; TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
; TITLE OF INVENTION: Fungi
; FILE REFERENCE: 1716.0340004
; CURRENT APPLICATION NUMBER: US/10/286,993
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/120,804
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/FI97/00037
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: US 08/590,563
; PRIOR FILING DATE: 1996-01-26

```

Matches	226;	Conservative	0;	Mismatches	163;	Indels	3;	Gaps
QY	893	AACATGTCATATAAACTACGAGCAAACTTCCAAACCAATGTAATGCTATTTATGCTC	952					
DB	191	AATAAGGTGATCAACTTCTCTGGATCTTATAATCCGAATGGAATTCATCTTAAGGCTC	250					
QY	953	TATGTTGGACTGTTGACCCCTCTTGTGCAATATTTATTTGCGACACTTGGGCAACTGG	1012					
DB	251	TATGGCTGCTCTAGAAACCCCACTGATTGAATATTACATTTGCGAAAATTTTCGGTACCTAC	310					
QY	1013	CGTCC--ACCAGGAGCAACGCCCTAAAGGGGACCACTCACTGTTGATGGAGAACATATCAT	1069					
DB	311	AATCCGAGTACCGGGCCCAAAAATTAGGCGAAGTCACCTAGTGATGATCGGTATATGAT	370					
QY	1070	ATCTACGAGACTCTTTAGAGTCAATCAACCCCTCCATTTAAGGGGATGCGACATTTTAAACAA	1129					
DB	371	ATCTACCGTACCAACGGCTTAATCAGCCATCGATCTTGAACCGCCACCTTTTATCAG	430					
QY	1130	TATTCGAGTGTTCGAAGATCGAAAGCGACGAGTGCACGATTTCTGTGACGCAACCACTTT	1189					
DB	431	TACTGGAGTGTTCGACGTAATCATCGGAGCTCCGGTTCCGTTAATCTGCGATCACTTT	490					
QY	1190	ACAGCGTGGGAAAACCTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTA	1249					
DB	491	AATGATGGCACAGCAAGGGTTAACCCCTAGTACATGGATTTATCAAATCGTAGCGGTG	550					
QY	1250	GAAGCGTATCAAGTAGCGGAAGTCTTAATGT	1281					
DB	551	GAAGGCTACTTCTCGATGGTTCCGCTAGTAT	582					
RESULT 12								
US-10-213-990-71								
; Sequence 71, Application US/10213990								
; Publication No. US20030082595A1								
; GENERAL INFORMATION:								
; APPLICANT: Jiang, Bo								
; APPLICANT: Bussey, Howard								
; APPLICANT: Stowers, Reg								
; APPLICANT: Roemer, Terry								
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL								
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE								
; FILE REFERENCE: 10182-019-999								
; CURRENT APPLICATION NUMBER: US/10/213,990								
; CURRENT FILING DATE: 2002-08-05								
; NUMBER OF SEQ ID NOS: 72								
; SOFTWARE: FastSeq for Windows Version 4.0								
; SEQ ID NO 71								
; LENGTH: 942								
; TYPE: DNA								
; ORGANISM: Aspergillus								
; FEATURE:								
; NAME/KEY: CDS								
; LOCATION: (1)... (942)								
US-10-213-990-71								
Query Match 7.4%; Score 111.4; DB 14; Length 942;								
Best Local Similarity 57.0%; Pred. No. 4.7e-16;								
Matches 224; Conservative 0; Mismatches 166; Indels 3; Gaps 1;								
QY	882	AACAAGTGTGTAACTGTCATATAAAGTACGAGGCAACTTCCAAACCAATGTAATGCTC	941					
DB	257	ATCCAGGAGTGACCATGACATTTCTCTCTGGCAGCTTCAATCTTCCGGAATGCTT	316					
QY	942	ATTATGCGTCTATGTTGACCTCTTGTGCAATATTTATTTGTCGACAGTT	1001					
DB	317	ACCTGTCGGTGTATGATGAGTACCAACCCCTCTAGTCAATCTACCTCTCGAGACT	376					
QY	1002	GGGCA---ACTGCGCTCCACAGGAGCAACGCTTAAGGGGACCACTCATCTGTTGAGGAG	1058					
DB	377	ATGGCAGTTACATCTCTGCTGGGCAATGACGCAACGGGCGCTCACCAGCGATGAT	436					
QY	1059	GAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAGGGGATTTGCCA	1118					

```
Db 437 CCACCTACGACATCTATGAGCAACCAACAGTCAACAGCCTTCGATCGTCGCGCACGGCA 496
Qy 1119 CATTTAAACAATATGGAGTGTTCGAGATCGAAACGACGAGTGGCAGCATTTCTGTCA 1178
Db 497 CCTTCAACCAATACTGTGTCATCCGCGCAAAACAAGCGATCCAGCGGCACAGTCACACCG 556
Qy 1179 GCACCCACTTTAGAGCGTGGGAAAACCTTAGGAGTGAATATGGGAAAATGTATGAGTCG 1238
Db 557 CGAATCACTTCAGGCTGGCTAGTCTGGGATGAACCTGGTACCCATACTACTCAGA 616
Qy 1239 CGCTTACTAGAGGCTATCAAGTAGCGGAA 1271
Db 617 TTGTTTCCACTGAGGATATGAGACGCGGTA 649

RESULT 13
US-10-213-990-70
; Sequence 70, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-70

Query Match 7.3%; Score 110; DB 14; Length 1002;
Best Local Similarity 57.8%; Pred. No. 1e-15;
Matches 216; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

Qy 901 CATAAATACGAGGCAACTTCCAAACCAATGGTAATGCGTATTTATGCGTCTATGGTTG 960
Db 336 CATTACCTTCTGTCGAGCTTCAATCCTTCGGAATGCTTACCTGTCGCTGATGATG 395
Qy 961 GACTGTGACCTCTTGTGCAATATATATGTCACAGTGGGCA---ACTGCGCTCC 1017
Db 396 GACTACCAACCCCTAGTGAATCTACATCTCGAGAACTATGCGAGTACAATCCTGG 455
Qy 1018 ACCAGGACCAAGCCTTAAGGGGACCATCACTGTTGATGGAGAACATATGATCTACGA 1077
Db 456 CTCGGGCATGACGACAGGGGACCGTCACAGCGATGATCCACTAGACATCTATGA 515
Qy 1078 GACTCTTAGAGTCAATCAACCTCCATTAAGGGGATGCCATTTAAACAATATPGAG 1137
Db 516 GCACCAACAGGTCAACAGCCTTCGATCGTCGCGCACGCCACTTCAACCAATACTGTC 575
Qy 1138 TGTTGAGATCGAAACGACGAGTGGCAGATTTCTGTACGACCACTTAGAGCGTG 1197
Db 576 CATCGGCCAAAACAAGCGATCCAGCGGCACAGTCCACCGCGAATCACTTCAAGGCGTG 635
Qy 1198 GAAAACCTTAGGATGAATATGGGAAAATGTATGAGTCGCGCTTACTGTAGAGGCTA 1257
Db 636 GCGTAGTCTGGGATGAACCTGGGTACCCATACTATCAGATTGTTTCCACTGAGGATA 695
Qy 1258 TCAAAGTAGCGGAA 1271
Db 696 TGAGACGACGGTA 709
```

RESULT 14
US-10-213-990-68

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; Sequence 68, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; NAME/KEY: CDS
; LOCATION: (1)...(705)
US-10-213-990-68

Query Match 7.2%; Score 108.8; DB 14; Length 705;
Best Local Similarity 51.9%; Pred. No. 1.7e-15;
Matches 298; Conservative 0; Mismatches 267; Indels 9; Gaps 2;

Qy 706 CGTCACCGACAATTCCTATGSCAACACGATGGCTATGATTAATTTTGAAGATAG 765
Db 120 CGGCACCCCAAGCTCCACCGCTCGAAACAACGGCTACTACTCTCTCTGGACTGAG 179
Qy 766 CGGTGGCTCTGGGACAATGATTCATCATGCGGCTAGCTTCAGTGCCTCAATGGAACA 825
Db 180 CGCGCGCAGCTGACCTACCAATGGCGCGGTGCTGCTACTCGCTCACTCGAGGA 239
Qy 826 TGTTAAACAACATATTTTCGTAAGGTAAATAATTCATGAAACACACACACCAACA 885
Db 240 CGTGGCAACTTTGTCGTGGGAAAGGC-----TGAACCCCTGGAAGCGTAGTACCG 293
Qy 886 AGTTGGTAACATGCTCATTAACCTACGAGCGCAACTTCCACCAATGGTATGCGTATTT 945
Db 294 AGCTTTAAGTAGAACCACTCAACTACGAGGCGAGCTTCAACCCGCGCAATGGCTACCT 353
Qy 946 ATGCGTCTATGTTGGACTGTTGACCTCTTGTGCAATATATATTGTCGACAGTTGGGG 1005
Db 354 GGCTGTCTACGCTGGACCAACCCCTTGATTGAGTACTACGTTGTTGAGTCGTATGG 413
Qy 1006 CAATGCGGTCACCA---GGAGCAACGCTTAAGGGGACCATCACTGTTGATGAGGAAC 1062
Db 414 TACATACAACCCCGCGAGCGCGGTACTCTCAGGGGCACTGTCAACACCGCGTGGCAC 473
Qy 1063 ATATGATATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATGGCCACATT 1122
Db 474 TTACAACATCTACACGCGCGTTCGCTCAATGCTCCCTCCATCGAAGGCACCAAGACCTT 533
Qy 1123 TAAACAATTTGGAGTGTTCGAAGATGAAACGACGAGTGGCAGCACTTTCTGTGAGCAA 1182
Db 534 CACCCAGTACTGCTGTGCGCACTTCAAGCGTACCGGGGCACTGTCAACATGGGCAA 593
Qy 1183 CCATTTAGAGCGTGGGAAACCTTAGGATGAATATGGGAAAATGTATGAGTGGCGCT 1242
Db 594 CCATTTCAACGCTTGGAGCAGACTGGGCGATGAACCTGGAACTCACAACCTACAGATTGT 653
Qy 1243 TACTGTAGAGGCTATCAAGTAGTCGGAAGTGT 1276
Db 654 CGCCACTGAGGTTTACCAGAGCAGCGGATCTGCT 687

RESULT 15
US-10-299-393-1
; Sequence 1, Application US/10299393
; Publication No. US20030108642A1
; GENERAL INFORMATION:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 10, 2004, 16:24:32 ; Search time 6558.71 Seconds
(without alignments)
8406.125 Million cell updates/sec

Title: US-09-909-207-10
Perfect score: 1513
Sequence: 1 AAATTGAATTGGTATATCT.....TGAAACACCTCGTCACTAG 1513

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98.6	6.5	618	7	CF472462 RTDS1_9 C
2	93	6.1	728	7	CN132941 OX1_9_D10
3	93	6.1	772	7	CN133022 OX1_9_D10
4	91.8	6.1	744	7	CF867983 trico13xe
5	91.8	6.1	799	6	CB898036 trico13xe
6	86.6	5.7	738	6	CD464145 ETH1_48 B
7	83.4	5.5	921	6	CD458837 Fg08_04B1
8	82.8	5.5	603	8	AQ160513 mgxb0006C
9	82.2	5.4	670	8	AQ447125 mgxb0005C
10	82.2	5.4	720	8	AQ361561 mgxb0004B
11	82.2	5.4	750	8	AQ160254 mgxb0003L
12	81.6	5.4	786	8	AQ325248 mgxb00021M
13	81.4	5.4	583	8	AQ399120 mgxb0001B
14	79.8	5.3	1101	9	AL057419 Drosophila
15	76.6	5.1	561	1	AQ396475 mgxb0010M
16	76.4	5.0	617	1	AJ638869 AJ638869
17	76.2	5.0	768	7	CF881056 trico083xj
18	76.2	5.0	822	6	CB907827 trico083xj
19	74.6	4.9	753	8	AQ448084 mgxb0016B
20	74.4	4.9	418	8	AQ398756 mgxb0005L
21	71.8	4.7	746	6	CB901964 trico028xi
22	71.8	4.7	746	7	CF871731 trico028xi
23	71.4	4.7	1101	9	AL063921 Drosophila
24	69.8	4.6	520	5	BQ165950 WHE0821-0

c	25	67.6	4.5	1101	9	CNS00EVL	AL069706 Drosophila
c	26	66.2	4.4	561	5	BQ471960	CD471960 HV04A02r
c	27	63.2	4.2	473	6	CD464005	ETH1_48 B
c	28	62	4.1	1101	9	CNS0021J	AL061936 Drosophila
c	29	61	4.0	939	6	BY720774	BY720774 BY720774
c	30	60.6	4.0	1101	9	CNS00EVL	AL069706 Drosophila
c	31	60.4	4.0	483	5	BQ664593	BQ664593 HV04A02u
c	32	60.2	4.0	1068	8	CC263147	CC263147 CH261-168
c	33	58.4	3.9	1101	9	CNS000D1	AL065414 Drosophila
c	34	57.2	3.8	1147	6	CD387645	CD387645 AGENCOURT
c	35	56.4	3.7	1031	9	CNS00CF2	AL059199 Drosophila
c	36	56	3.7	1001	9	CNS01400	AL103554 Drosophila
c	37	54.8	3.6	886	8	BH177277	BH177277 008_L_22-
c	38	54.8	3.6	886	9	CNS07JUX	AL614235 T3 end of
c	39	54.8	3.6	1101	9	CNS00807	AL069440 Drosophila
c	40	54.6	3.6	843	9	CNS00CS1	AL059666 Drosophila
c	41	54.6	3.6	958	9	CNS04RNK	AL304134 Tetraodon
c	42	54.4	3.6	1092	9	CNS020K7	AL175696 Tetraodon
c	43	54.2	3.6	1043	9	CNS0145P	AL103735 Drosophila
c	44	54	3.6	928	9	CNS00DKY	AL071865 Drosophila
c	45	54	3.6	928	9	CNS00DKY	AL071865 Drosophila

ALIGNMENTS

RESULT 1
CF472462
LOCUS
DEFINITION
RTDS1_9 C03.g1_A015 Drought-stressed loblolly pine roots DS1 Pinus taeda cDNA clone RTDS1_9_C03_A015 5', mRNA sequence.
ACCESSION
CF472462
VERSION
CF472462.1 GI:34489834
KEYWORDS
EST.
SOURCE
Pinus taeda (loblolly pine)
ORGANISM
Pinus taeda
REFERENCE
1 (bases 1 to 618)
AUTHORS
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.
TITLE
An EST database from drought-stressed loblolly pine (Pinus taeda) roots
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: RTDS1_9 C03.b1_A015
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@cuga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).
FEATURES
1..618
Location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTDS1_9 C03 A015"
/lab_host="DH10B-T1 phage-resistant E. coli"
/notes="Vector: pSL180; Site 1: EcorI; Site 2: XhoI; The library was prepared from polyA+ RNA from drought-stressed loblolly pine (Pinus taeda) roots. Water was withheld from

ramet clones until predawn needle water potential reached -1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSul180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

```

Query Match      6.5%; Score 98.6; DB 7; Length 618;
Best Local Similarity 57.4%; Pred. No. 2.8e-12;
Matches 198; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 882 AACAAAGTTGGTAACATGTCCATAAATCTACGAGCAACTTCCAAACCAATGTAATGCT 941
   |||||
Db 254 ATCCAGGTAGTCGCGAGACATCACTTCTCGGTACCTTCAGCCCGCAGCAAGCGCT 313
   |||||
QY 942 ATTATGCGTCTATGGTGGAGCTGTGACCCCTCTTGTGCGAATATATATGTCGACGTT 1001
   |||||
Db 314 ATCTTGGCGTCTACGGCTGGACCAACGACCCCTCTGATCGAATACATTTCTGAAAGCT 373
   |||||
QY 1002 GGGCAACTGGGCTCC---ACCAGAGCAACGCTTAAGGGACCATCACTGTTGATGGAG 1058
   |||||
Db 374 ATGGGACCTACAAACCTTGATCCAGATGACCATATGGGCACTGTCAACGACGGTG 433
   |||||
QY 1059 GAACATATGATCTACGAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGATTGCCA 1118
   |||||
Db 434 CGACCTATGATCTATGAGCAGCAAGTCAACAGCCCTCTATCTGCGCAGCGGA 493
   |||||
QY 1119 CATTAAACATATTTGGAGTGTGGAAGATCGAAGCAACGACGAGTGGCAGATTTCTGTCA 1178
   |||||
Db 494 CTTTCAACCAATATCTGCTCCATCCCTGACAGCAAGCGGTCCAGCGGAATGTCACTACAG 553
   |||||
QY 1179 GCAACCACTTTAGAGCGTGGGAAACTTTAGGATGAATATGGGA 1223
   |||||
Db 554 CGAACCAATTCAACGCTGGGCTGCTTGGGCATGAACCTGGGGA 598
   |||||

```

RESULT 2

```

CN132941
LOCUS      CN132941
DEFINITION OX1_9_D10.bl_A002 Oxidatively-stressed leaves and roots Sorghum
            bicolor cDNA clone OX1_9_D10_A002 3', mRNA sequence.
ACCESSION CN132941
VERSION    CN132941.1 GI:45963408
KEYWORDS   EST.
SOURCE     Sorghum bicolor (sorghum)
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE  1 (bases 1 to 728)
            Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C.,
            Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H.
            An EST database from Sorghum: oxidatively stressed leaves and roots
            Unpublished (2003)
Other ESTs: OX1_9_D10.gi_A002
Contact: Cordonnier-Pratt MW
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug3-14 (TAGCTAGCGCGCGGACCC)
POLYA=Yes.

```

FEATURES

Location/Qualifiers

source

```

1. 728
/organism="Sorghum bicolor"
/multi_type="mRNA"
/cultivar="Brix623"
/db_xref="taxon:4558"
/clones="OX1_9_D10_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Oxidatively-stressed leaves and roots"
/notice="Organ: Leaf and Root; Vector: pME18S-FL3; Site: 1:
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 uM methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all
tissue pooled. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites of the
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTC,
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
insert."

```

ORIGIN

```

Query Match      6.1%; Score 93; DB 7; Length 728;
Best Local Similarity 53.9%; Pred. No. 5.8e-11;
Matches 214; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

QY 900 CCATAAATCTACGAGCCAACTTCCAAACCAATGTAATGCTATTTATGCTCTATGCTT 959
   |||||
Db 101 CCATCAACTATGGCGGTTCTTTTCAGCCCTCAGGGTAAAGGCTACTCTCTGCGCTACGGCT 160
   |||||
QY 960 GGACTGTTGACCTCTTGTGCAATATATATTTGTCAGACTTGGGCA---ACTGGCGTC 1016
   |||||
Db 161 GGACTCGAGCCCTCTGTTGAGTACTACGTCATCGAGAACTACGGCACTTACAACTG 220
   |||||
QY 1017 CACCAGGAGCAACGCTTAAGGGACCATCACTGTTGATGGAGGAACATATATATCTACG 1076
   |||||
Db 221 GCTCTGCTGGCCAGCACAAGGGCCCGTCTACAACGCGGCACACCTACGATCTCTACC 280
   |||||
QY 1077 AGACTCTTAGAGTCAATCAACCTCCATTAGGGGATGCCACATTTAAACAATATGGA 1136
   |||||
Db 281 AGACCAACCCGTACAACACGACGCCCTCTATCGACGCGCAACAGACCTTCAACAGTACTGGG 340
   |||||
QY 1137 GTGTTGGAAGATCGAAACGACGAGTGCAGATTTCTGTGACGAACCACTTTTAGAGCGT 1196
   |||||
Db 341 CCATCCCGCCCAACAGCGCAGAGCGGCGGTCAACATCGACATCTTCAATGTT 400
   |||||
QY 1197 GGGAAAATTTAGGATGAATATGGGAAAATGTATGAAGTCGCGCTTACTGTAGAGGCT 1256
   |||||
Db 401 GGGCTAACGCTGATGAGACTTGGAAACCACTACTACAGATCCTGCTACCGAGGAT 460
   |||||
QY 1257 ATCAAGTAGCGGAAGTCTTAATCTATATAGCAATAC 1293
   |||||
Db 461 ACCAGAGCAGTGGATCTTCTTCTATCTATGTCCAGAC 497
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```

RESULT 3

```

CN133022
LOCUS      CN133022
DEFINITION OX1_9_D10.gi_A002 Oxidatively-stressed leaves and roots Sorghum
            bicolor cDNA clone OX1_9_D10_A002 5', mRNA sequence.
ACCESSION CN133022
VERSION    CN133022.1 GI:45963542
KEYWORDS   EST.
SOURCE     Sorghum bicolor (sorghum)
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE  1 (bases 1 to 772)
            Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C.,
            Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H.
            An EST database from Sorghum: oxidatively stressed leaves and roots
            Unpublished (2003)

```

COMMENT

Other ESTs: OX1.9.D10.b1.A002
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 563 0210
 Email: mmpratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.
 Seq primer: Sug5 (CTTCTGCTCTAAAGTGGC).

FEATURES

Source

1. .772
 Location/Qualifiers
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTX623"
 /db_xref="taxon:4558"
 /clone="OX1.9.D10.A002"
 /lab_host="DH10B-Ti phage-resistant E. coli"
 /clone_lib="Oxidatively-stressed leaves and roots"
 /note="Organ: Leaf and Root; Vector: pME18S-FL3; Site: 1:
 XhoI; Site 2: XhoI; The library was prepared from polyA+
 RNA from oxidatively stressed, hydroponically grown
 sorghum seedlings. At 8 days of age, growth medium was
 supplemented with hydrogen peroxide to 0.003% and leaves
 were misted with 10 uM methyl viologen. Leaves and roots
 were harvested at 3, 12 and 27 hr after treatment and all
 tissue pooled. Double-stranded cDNA was cloned
 unidirectionally into different DraIII sites of the
 pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,
 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
 insert."

ORIGIN

Query Match 6.1%; Score 93; DB 7; Length 772;
 Best Local Similarity 53.9%; Pred. No. 5.9e-11;
 Matches 214; Conservative 0; Mismatches 180; Indels 3; Gaps 1;
 QY 900 CATAAATACGAGGCAACTTCAACCAATGTAATGCGTATTTATGCGTCTAGGTT 959
 Db |||||
 324 CCATCAACTATGCGGGTTCTTTCAGCCCTCAGGGTAAACGGCTACCTCTGCGTCTACGGCT 383
 QY |||||
 960 GGACTGTGACCTCTGTGCGAATATTATTTCTGACAGTTCGGGCA--ACTGGCGTC 1016
 Db |||||
 384 GGACTCGAGCCCTCTCGTTGAGTACTACGTATCGAGAACTACGGCACTTACACCTG 443
 QY |||||
 1017 CACGAGGCAACGCTTACGGGACCATCTCTTGTATGGAGGAACATATGATCTACG 1076
 Db |||||
 444 GCTCTGTCGACGACAGGCGACCGCTCTACACGAGCGGACACTACGACTCTTACC 503
 QY |||||
 1077 AGACTCTTGAAGTCAATCAACCTTCATTAAGGGATGCGCATTTAAACATATTGA 1136
 Db |||||
 504 AGACCAACCCCTACACAGCCCTCTATCGACGGCCCAACAGACGCTTCAACCACTACTGGG 563
 QY |||||
 1137 GTCTTGAAGATCGAAGCGACGAGTGGACGATTTCTGTGACCAACCACTTTTAGAGCGT 1196
 Db |||||
 564 CCATCGCGCGCAACAAGCGAGAGCGCGCGCTCAACATGCGAGACTATCTTCATGCTT 623
 QY |||||
 1197 GGGAAACTTTAGGATGAATATGGGAAAAATGTATGAAGTTCGGGCTTACTGTAGAGGCT 1256
 Db |||||
 624 GGGCTAACGCTGTATGAGACTTGGAAACCACTACTACAGATCCTTGCTACCGAGGAT 683
 QY |||||
 1257 ATCAAGTACGGAAGTGTAAATGTATATAGCAATAC 1293
 Db |||||
 684 ACCAGACGTGGATCTTCTTCTATCTATCTATGTCAGAC 720

RESULT 4

CF867983 744 bp mRNA linear EST 31-OCT-2003
 trico13xe09.b1 T.reesei mycelial culture, Version 6 October 2003
 DEFINITION Hypocrea jecorina cDNA clone trico13xe09, mRNA sequence.
 CF867983
 ACCESSION CF867983
 VERSION
 KEYWORDS
 SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
 ORGANISM Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 REFERENCE 1 (bases 1 to 744)
 AUTHORS Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
 Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
 Ward,M. and Dean,R.A.
 TITLE Characterization of the protein processing and secretion pathways
 in a comprehensive set of expressed sequence tags from Trichoderma
 reesei
 JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
 COMMENT Contact: Ralph A. Dean
 Fungal Genomics Laboratory
 North Carolina State University
 Campus Box 7251, Raleigh, NC 27695, USA
 Tel: 919-513-0020
 Fax: 919-513-0024
 Email: ralph.dean@ncsu.edu
 Seq primer: Lr-Fl primer
 Location/Qualifiers
 1. .744
 /organism="Hypocrea jecorina"
 /mol_type="mRNA"
 /strain="QM6a"
 /db_xref="taxon:51453"
 /clone="trico13xe09"
 /dev_stage="mycelia"
 /clone_lib="T.reesei mycelial culture, Version 6 October
 2003"
 /note="Vector: pRFP3Y; Site 1: Not I/Sal I; Mycelial
 culture grown from 24 hrs to 6 days with varying Carbon
 and Nitrogen sources and concentrations."

ORIGIN
 Query Match 6.1%; Score 91.8; DB 7; Length 744;
 Best Local Similarity 55.0%; Pred. No. 1.1e-10;
 Matches 202; Conservative 0; Mismatches 162; Indels 3; Gaps 1;
 QY 893 AACATGTCATAAATACGAGCCAACTTCCAAACCAATGGTAATCGGTATTTATGCGTC 952
 Db |||||
 353 AACAGGTTCATCAACTTCTCGGGCAGCTACACCCCAACGGCAACAGCTACCTCTCCGTG 412
 QY |||||
 953 TATGTTGGACTGTTGACCCCTTTGTCGAATATTATTTGTCACAGTTGGGGCAACTGG 1012
 Db |||||
 413 TAGCGTGTCCCGCAACCCCTTGATCGAGTACTATCGTCGAGAACTTTGGCACTAC 472
 QY |||||
 1013 CGTCCACCA---GGAGCAACGCCAAGGGGACCATCACTGTTGATGGAGGAACATATGAT 1069
 Db |||||
 473 AACCGTTCACGGGCGCCACCAAGCTGGCGAGGTCACTCCGACGGCAGCTACGAC 532
 QY |||||
 1070 ATCTACGAGACTTTAGAGTCAATCAACCTTCATTAAGGGGATTCGCACATTTAAACAA 1129
 Db |||||
 533 ATTTACCGGAGCGGCGGTCAACCAAGCGCTCCATCATCGGCACCGCCACTTTTACCAG 592
 QY |||||
 1130 TATTGAGTGTTCGAGATCGAAACCGACGAGTGGCACGATTTCTGTACGACCAACCACTTT 1189
 Db |||||
 593 TACTGTCTCGTCGCGCGCAACCACTCGTCTGAGGGTCCGTCACACGGCGAACCCTTC 652
 QY |||||
 1190 AGAGCGTGGGAAACTTAGGGATGAATATGGGAAAAATGTATGAAGTTCGCGCTTACTGTA 1249
 Db |||||
 653 AACCGTGGGCTCAGCAAGGCCTGACGCTCGGACGATGATACCAGATTGTTGCCGTG 712
 QY |||||
 1250 GAAGGCT 1256

Db 345 CCATCAAGTACTCTGTTACTTACACATCAACGAAACAGCTACCTCGCTGTTTACGGAT 404

QY 960 GGACTGTTGACCTCTTGTGCAATATATATTTGTGACAGTTGGGGCACTGGCGTCCAC 1019

Db 405 GGACTCAGAACCTCTCTCATCGAGTACTACATCGTTGAGAACTTCGGCACCTCAACCCCT 464

QY 1020 CA--GGACCAACGCTAAGGGGACCATCACTGTTGTGATGGAGAACATATATATCTAGC 1076

Db 465 CTTCCGGCGCCGAGAAAGGTTGAGTCACTGTTGACGGATCTGTCTACGACATCTAGC 524

QY 1077 AGACTCTTAGAGTCAATCAACCTCCATTAAGGGATTCACATTTAAACAATATGGA 1136

Db 525 TCAGCACCCGTTGCAACGCCCCCTCCATTTAGGGTAAACAAGACCTTTTACGACGATCTGCT 584

QY 1137 GTGTTGCAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACGACCACTTTTAGAGCT 1196

Db 585 CTGTTGCGACCAACAAGCGATCCAGCGGATCCCGTCAACACCGGTGCTCACTTCCAGGCT 644

QY 1197 GGGAAACTTAGGATGAATATGGGAAATATGATCAAGTCCGCGCTTACTGTAGAGGCT 1256

Db 645 GGAATAATGTGGCCCTCACTTGGTAAACCAACTATCAGATCTTGTGTTGAGGCT 704

QY 1257 ATCAAGTAGCGGAAGTGCTA 1277

Db 705 ACTACAGCTGGCTGCGCA 725

RESULT 7

CD458837 921 bp mRNA linear EST 14-JUN-2004

LOCUS Fg08_04b10.A Fg08_AAPC_ECORC_Fusarium_graminearum_complex_substrate

DEFINITION Gibberella zeae cDNA clone Fg08_04b10, mRNA sequence.

ACCESSION CD458837 GI:31373577

VERSION EST.

KEYWORDS Gibberella zeae

SOURCE Gibberella zeae

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 921)

AUTHORS Watson,R.J., Heyes,R., Chapados,J., Couroux,P., Harris,L.J., Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A., Spriet,D. and Tinker,N.A.

TITLE A cDNA library prepared from Fusarium graminearum grown on a complex plant substrate

JOURNAL Unpublished (2003)

COMMENT Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.

FEATURES

source

1..921

/organism="Gibberella zeae"

/mol_type="mRNA"

/strain="DAOM 180378"

/db_xref="taxon:5518"

/clone="Fg08_04b10"

/tissue_type="Mycelium"

/dev_stage="Asexual"

/lab_host="E. coli DH10B"

/clone_lib="Fg08_AAPC_ECORC_Fusarium_graminearum_complex_substrate"

/note="Vector: pBluescript II+; Site 1: EcoRI; Site 2: XhoI; Fusarium graminearum grown on a complex plant substrate-- wheat leaves treated to remove most of the low molecular weight, water-soluble components."

ORIGIN

Query Match

5.5%; Score 83.4; DB 6; Length 921;

Best Local Similarity 52.4%; Pred. No. 1.1e-08;

Matches 208; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 900 CCATCAAGTACTCGGAGCCAACTTCCAAACCAATGTAATGCGTATTTATGCGTCTATGGTT 959

Db 363 CCATCAAGTACTCGGAGGTTCCCTTCAACCTCAGGGTAACGGATACCTTTCGGTTACGGAT 422

QY 960 GGACTGTTGACCCCTCTTGTGCAATATATATTTGTGCGAGTTGGGGCACTGGCGTCCAC 1019

Db 423 GGACCCGGTCCCTCGTCGAGTACTAGTCAATCGAGAGTTACGGTTCTTACAACCCCG 482

QY 1020 CAGGA---GCAACGCTAAGGGGACCATCACTGTTGATGGAGAACATATATATCTAGC 1076

Db 483 CGAGCCAGGCTCAGCACCGAGGTACCGTCTACACGACGGTGACACCTACGATCTCTATA 542

QY 1077 AGACTCTTAGAGTCAATCAACCTCCATTTAAGGGATTCGACATTTAAACAATATGGA 1136

Db 543 TGTCCACCGCTTACCAACAGCCTTCGTCGACGGTGTTCAGACCTTCAACGAGTACTGGT 602

QY 1137 GTGTTGCAAGATCGAAACGACGAGTGGCAGCATTTCTGTGACGACCACTTTTAGAGCT 1196

Db 603 CCATCGCGCGCAACGAGGTACCGGCTCGTCAACATGCGAAGCACTTCAATGCTT 662

QY 1197 GGGAAACTTAGGATGAATATGGGAAATATGTAAGTCCGCTTACTGTAGAGGCT 1256

Db 663 GGAGATCTGCTGGCATGAACCTCGGAAACCACTACTACCAGATTCTGGCCACTGAGGGTT 722

QY 1257 ATCAAGTAGCGGAAGTCTAATGATATATAGCAATAC 1293

Db 723 ACCAGAGCAGTGGCTCATCTTCTATCTATGTCCAGAC 759

RESULT 8

LOCUS AQ160513/c

DEFINITION clone mgxb0006C21r CUGI Rice Blast BAC Library Magnaporthe grisea genomic survey sequence.

ACCESSION AQ160513

VERSION AQ160513.1 GI:3557502

KEYWORDS GSS.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Magnaporthe grisea

REFERENCE 1 (bases 1 to 603)

AUTHORS Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M., Wing,R.A. and Dean,R.A.

TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome

JOURNAL Unpublished (1998)

COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293

Seq primer: GGAACAGCTATGACCATG

Class: BAC ends

High quality sequence stop: 424.

Location/Qualifiers

1..603

/organism="Magnaporthe grisea"

/mol_type="genomic DNA"

/strain="70-15"

/db_xref="taxon:148305"

/clone="mgxb0006C21r"

/tissue_type="Protoplasts"

/lab_host="E. coli DH10B"

/clone_lib="CUGI Rice Blast BAC Library"

/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with

FEATURES

source

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

Query Match 5.5%; Score 82.8; DB 8; Length 603;
 Best Local Similarity 52.8%; Pred. No. 1.4e-08;
 Matches 227; Conservative 0; Mismatches 197; Indels 6; Gaps 2;

QY 854 AAAAATTCATGAACACACACACACAAAGTTGGTATACATGTCATTAACCTACGGA 913
 DB 444 AAAAAAAGAGACTACCAACACACACACAAAGCGCGTCTCACTACTCG 385

QY 914 GCCAACTTCCAAACCAATGTAATCGGTATTTATCGGTCTATGGTTGGACTGTTGACCGT 973
 DB 384 GCGAGTACAGCCCCAGGCACTCATACCTGGCGGTCTAGCGTGGAGCGCAACCG 325

QY 974 CTTGTCGAATATATATTGTGACAGTTGGGGCAACTGCGGTCCACCA---GGAGCAAG 1030
 DB 324 CTGATCGAGTACTACGTGTGAGAGCTTTGGCAGCTACAAACCGCTCGCGGCGCCACC 265

QY 1031 CCTAAGGGACCATCAGTGTGATGGAGACATATGATATCTACGAGACTCTTAGAGTC 1090
 DB 264 AACCGCGGTCTTCACTTCGACGCGACCTACGACATCTCGTTCAGCAACCGCTAC 205

QY 1091 AATCAACCTCCATTAAGGGATTGCCACATTTAAACAATATGAGTGTTCGAAGATCG 1150
 DB 204 AACGAGCTTCATCGACGCGCAAGACCTTTAGAGTCTGTCGTCGCGCGCAAC 145

QY 1151 AAACGACAGTGGCAGCATTTCTGTGACAACTCTTAGAGCGTGGGAAACTTAGGG 1210
 DB 144 AAGCGCGCAGCGGACCGTCACTTTTGCCAAACAGTCAACGCGCTGGCGCAACCGCGGC 85

QY 1211 ATGATATGGGAAATATGTAAGTTCGCG---CTTACTGTAGAGGCTATCAAGTAGC 1267
 DB 84 CTCACCTCGGCAACAGTGGAACTACAGATCTTGACCGTTCGAGGGCTACCAAGCAGC 25

QY 1268 GGAAGTGCTA 1277
 DB 24 GGCCTCGCCA 15

RESULT 9
 AQ447125/c
 LOCUS
 DEFINITION
 clone mgxb0005C20f, CUGI Rice Blast BAC Library Magnaporthe grisea genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 COMMENT

Unpublished (1998)
 Contact: Dean RA
 Clemson University
 Clemson University
 100 Jordan Hall,
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: TAATACGACTCTACTATAGG

Class: BAC ends
 High quality sequence stop: 263.
 Location/Qualifiers
 1..670

/organism="Magnaporthe grisea"
 /mol_type="genomic DNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0005C20f"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice Blast BAC Library"
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."

ORIGIN

Query Match 5.4%; Score 82.2; DB 8; Length 670;
 Best Local Similarity 54.6%; Pred. No. 2e-08;
 Matches 209; Conservative 0; Mismatches 168; Indels 6; Gaps 2;

QY 901 CATAAATACGAGGCCAACTTCCAAACCAATGGTAAATGCGTATTTATGCGTCTATGGTTG 960
 DB 397 CATCAACTACTCGGCGAGCTACAGCCCGGCAACTCATACCTGGCGGTCTACGGCTG 338

QY 961 GACTGTTGACCCCTTGTGCAATATATATGTCGAGTTGGGCACTGGCGTCCACC 1020
 DB 337 GACGCGCAACCCGCTGATCGAGTACTACGTGGTGGAGAGCTTTGGCAGCTACAACCCGTC 278

QY 1021 A---GGAGCAACGGCTTAAGGGGACCATCCTGTTGATGGAGGAACATATGATATCTACGA 1077
 DB 277 GTCGGCGGCCAACCAACCGGGGTCTTCCACCTCGAGCGGACGACTTACGACATCTCGT 218

QY 1078 GACTCTTAGAGTCAATCAACCTCCATTAAGGGGATGCGCACATTTAAACAATATTGAG 1137
 DB 217 CAGCACCCGCTACCAACCAAGCCCTCCATCGACGCGCAACAGACCTTTACGACGTTCTGTC 158

QY 1138 TGTTCGAAGTCAAGACGACGAGTGGCAGCATTTCTGTCAGCAACCACTTTAGAGCGTG 1197
 DB 157 GGTGCGCGCAACAAAGCGCGCCAGCGGCACCGTCACTTTTCCCAACCACTCAACGCGTG 98

QY 1198 GGAATACTTAGGGATGAATATGGGGAATAATGATGAAGTCGCG---CTTACTGTAGAGG 1254
 DB 97 GCGCAACCGCGGCTCAACCTCGCAACCAAGTGGAACTTACAGATCTCTGCGCGTCCGAGG 38

QY 1255 CTATCAAGTAGCGGAAGTGCTA 1277
 DB 37 CTACCACAGCAGCGGCTCCGCCA 15

RESULT 10
 AQ361561/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AQ361561
 mgxb0004B19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0004B19r, genomic survey sequence.

AQ361561
 GSS.
 GI:4211400

Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.
 1 (bases 1 to 720)
 Yu.Y., Zhu.H., Boyd.C.A., Gaudette.B., Gayle.A., Kingsbury.R.,
 Phillips.K., Sasnowski.M, Wing.R.A. and Dean.R.A.

TITLE
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

JOURNAL
Unpublished (1998)

COMMENT
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 321.
Location/Qualifiers
1. .720
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0004B19r"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25x genome coverage. High density colony filters
are available upon request."

FEATURES
source

ORIGIN

Query Match 5.4%; Score 82.2; DB 8; Length 720;
Best Local Similarity 54.1%; Pred. No. 2e-08;
Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;

QY 848 AAGGTAATAAATTCATGAAACACAAACACCAACCAAGTTGGTAACATGTCCATAAAC 907
DB 445 AAGGTAATAAATTCATGAAACACAAACACCAACCAAGTTGGTAACATGTCCATAAAC 391
QY 908 TACGGAGCCAACTTCCAAACCAATGTAATGCGTATTTATGCGTCTATGTTGGACTGTT 967
DB 390 TACTCGGGCAGCTACAGCCNCAGGCAACTCATACCTGGCCGCTCTACGGCTGGACGCGC 331
QY 968 GACCCCTTTGCGAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACCA---GGA 1024
DB 330 AACCCGCTGATCGAGTACTACGTTGGGAGAGCTTTGGCAGCTACAAACCCGTGTCGGGC 271
QY 1025 GCAACGCTTAAGGGGACCATCCTGTTGATGGAGGAACATATGATATCTACGAGACTCTT 1084
DB 270 GCCACCAACCGCGGTCTTCACTCGGAGGAGAGCTTTGGCAGCTACAAACCCGTGTCGGGC 211
QY 1085 AGAGTCAATCAACCCCTCCATTAAGGGGATTCGCCAATTTAAACAATATTGGAGTTTCA 1144
DB 210 CGCTACAAACAGCCCTCCATCGAGCGGCAACAAAGACCTTTTCAGCAGTTCTGTCGGTCCG 151
QY 1145 AGATCGAAGCCAGAGTGGCAGCATTTCTGTCAGCAACCATTTAGAGCGTGGGAAAC 1204
DB 150 CGCAACAAGCGCGGCGGACCGCTCACCTTTGCCAACAACAGTCAACCCCTGGCGGAAC 91
QY 1205 TTACGGATGAATATGGGGAATATGTAAGTTCGCG---CTTACTGTAGAAGGCTATCAA 1261
DB 90 GCCGCGCTCACTTCGGCAACCACTGGAATACCAAGTCTGGCGGTGAGGCTACCAAC 31
QY 1262 AGTAGCGAAGTGCTA 1277
DB 30 AGCAGCGGCTCCGCCA 15

RESULT 11
A0160254/c
LOCUS
DEFINITION
mgxb0003L19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0003L19r, genomic survey sequence.
ACCESSION
A0160254
VERSION
A0160254.1 GI:3557243
KEYWORDS
GSS.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 750)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 344.
Location/Qualifiers
1. .750
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/mol_type="genomic DNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0003L19r"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25x genome coverage. High density colony filters
are available upon request."

FEATURES
source

ORIGIN

Query Match 5.4%; Score 82.2; DB 8; Length 750;
Best Local Similarity 54.1%; Pred. No. 2e-08;
Matches 236; Conservative 0; Mismatches 189; Indels 11; Gaps 3;

QY 848 AAGGTAATAAATTCATGAAACACAAACACCAACCAAGTTGGTAACATGTCCATAAAC 907
DB 445 AAGGTAATAAATTCATGAAACACAAACACCAACCAAGTTGGTAACATGTCCATAAAC 391
QY 908 TACGGAGCCAACTTCCAAACCAATGTAATGCGTATTTATGCGTCTATGTTGGACTGTT 967
DB 390 TACTCGGGCAGCTACAGCCNCAGGCAACTCATACCTGGCCGCTCTACGGCTGGACGCGC 331
QY 968 GACCCCTTTGCGAATATTATTTGTCGACAGTTGGGCAACTGGCGTCCACCA---GGA 1024
DB 330 AACCCGCTGATCGAGTACTACGTTGGGAGAGCTTTGGCAGCTACAAACCCGTGTCGGGC 271
QY 1025 GCAACGCTTAAGGGGACCATCCTGTTGATGGAGGAACATATGATATCTACGAGACTCTT 1084
DB 270 GCCACCAACCGCGGTCTTCACTCGGAGGAGAGCTTTGGCAGCTACAAACCCGTGTCGGGC 211
QY 1085 AGAGTCAATCAACCCCTCCATTAAGGGGATTCGCCAATTTAAACAATATTGGAGTTTCA 1144

blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

Query Match 5.4%; Score 81.4; DB 8; Length 583;
 Best Local Similarity 52.8%; Pred. No. 2.9e-08;
 Matches 200; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 854 AAAAAATTCATGAACACACACACACCAAGTTGGTAACATGTCATAACTACGGA 913
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QY 914 GCCAACTTCCAAACCAATGGTATGCTATTTATGCTGTATGGTTGGACTGTGACCT 973
 DB 385 GCGAGCTACGCCACAGGCACTCATCTGGCGTCTACGGTGGAGCGCAACCG 326

QY 974 CTGTGCAATATATATGTCGACAGTTGGGGCACTGGCGTCCACCA---GGAGCAAG 1030
 DB 325 CTGATCGAGTACTACGTGGGAGCTTTGGCAGCTACACCCGTCGTCGGCGCCACC 266

QY 1031 CCTAAGGGACCATCTGTTGATGGAGCAATATGATCTACGAGACTCTAGAGTC 1090
 DB 265 AACCGCGCTCTTCACTCGGACGCGACCTACGACATCTGTCGACGCCGCTAC 206

QY 1091 AATCAACCTTCCATTAAGGGATTGCGCATTTAAACAATATGGAGTGTTCGAAGATCG 1150
 DB 205 AACGAGCTTCCATCGACGCGCAGACCTTTCAGCAGTTCTGGTGGTGGCGCAAC 146

QY 1151 AACGCGCAGTGGCGACGATTTCTGTCAGCAACCTTTAGAGCGTGGGAACTTAGGG 1210
 DB 145 AAGCGCGCAGCGCACCGTCTTGGCAACCGCTCAACCGCTGGCGCAACCGCGC 86

QY 1211 ATGAATATGGGAAATGT 1229
 DB 85 CTCACCTCGGCAACAGT 67

RESULT 14

CNS00801/c
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence 17 end of BAC # BACR24D09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL057419.1 GI:4937885
 GSS.
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)

REFERENCE

Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR24D09"
 /clone_lib="RPCI-98"
 /note="end : 17"

ORIGIN

Query Match 5.3%; Score 79.8; DB 9; Length 1101;
 Best Local Similarity 38.7%; Pred. No. 7.6e-08;
 Matches 239; Conservative 75; Mismatches 296; Indels 7; Gaps 2;

QY 72 TCTTTATTAACGCTTAACCACTTGCATCTTATCAACAAGCAATCTCTTTATAGGAAGT 131
 DB 1097 TTTTMMTTTTWAATAAATAAATAATTAATTTTAAATTTTAAATTTTAAATTTTAA 1038

QY 132 CCATTTGCAAGACCAATAAATAATCTTTTCCCTATTTTATCTTATCGCTTGCCTG 191
 DB 1037 ATWATTAATATWATTTTAAAAAATAAATAATTTTAAATTTTAAATTTTAAATTT 978

QY 192 TTAATTTGTAACCTTTTATTTAGTTTACGTGATGTTCCCTCATTCATACCATTAATCA 251
 DB 977 TTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 919

QY 252 GTTAACGCTAGAGTCACTCTTTTTCGGTTTCTCAAAATAACCTGGAAGAACAATATG 311
 DB 918 ATATAAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 859

QY 312 ATTTTCTCAGCGCGTCCATAATGGAATATATATATCTCTTTTATACATTAAGTAAT 371
 DB 858 WATTAATAATTAATAWATWATATTTTATTTTATTTTATTTTATTTTATTTTATTT 799

QY 372 AGTATATATCTCGGTTATCAAAATGTGAGATAATCAATTAATGATCAAAACAGCAGT 431
 DB 798 TTTTWTTTTWTWATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 739

QY 432 AAAAAACACTGATGTTGACCTCTTAAAGAAGTGTCTATCTATGATGAAAAGATAATAT 489
 DB 738 AAAAAAATAATTTTATTAASVMTWKWASSSCAAATVTTWAAAAATAATSTAM 679

QY 490 ----CCAGTTTCAAAATTTGAAATAGTGTGATGGAATAGTTGATGCTCACTGCTG 545
 DB 678 AATSVCASBSVMTTATATTTTTTASAAAATAAATAATTTTGTGKGTGTTTTTADTT 619

QY 546 AAGAGGAGGTAGTAGTACGCTAGCTTCATTACCAAAATAGTTGTAAAAAATAA 605
 DB 618 SSATATTAATTSVTRATGTTDATTAAASAAAATAAAWKTTRAAAAAATAAATAA 559

QY 606 AGCAGGAATCCCTTAATGACAAAAGAAATGACGTTGATTTTACGCTTTTATAGTTGT 665
 DB 558 ARSATAAARAATAATTAATAAATAAATAATTTTGTGKGTGTTTTTADTTTADTT 499

QY 666 TTGCACTAACCTTACCT 682
 DB 498 ATTTNNNNNNNTTGST 482

RESULT 15

AQ396475/c
 LOCUS
 DEFINITION
 clone mgxb0010M14f CUGI Rice Blast BAC Library Magnaporthe grisea genomic survey sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AQ396475
 mgxb0010M14f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 clone mgxb0010M14f, genomic survey sequence.
 AQ396475
 GSS.
 Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaportha.
1 (bases 1 to 561)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome

Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAAATGACTACTATAGGG

Class: BAC ends

High quality sequence start: 50

High quality sequence stop: 443.

FEATURES

source

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/organism="Magnaporthe grisea"
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/strain="70-15"
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/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 5.1%; Score 76.6; DB 8; Length 561;
Best Local Similarity 53.7%; Pred. No. 3.9e-07;
Matches 204; Conservative 0; Mismatches 170; Indels 6; Gaps 2;

QY 839 TTATTCCGTAAAGTAAATAATTCATGAACACAAACACACCAACAGTTGGTAACATG 898
Db 495 TTTTCCCAAAAGGAAAGAAAAAGAGACTANCAACACCAACAAACAGCGCGGT- 437

QY 899 TCATAAACTACGGAGCAACTTCCAAACCAATGGTAATGCGTATTTATGCGTCTATGGT 958
Db 436 --CATCACTACTCGGGCAGCTAGAGCCCGCAGGCAACTATACCTGGCGGTCTACGGC 379

QY 959 TGGACTGTGACCTCTTTGTGCAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCA 1018
Db 378 TGGACCGCGCAACCCGCTGATCGAGTACTACGTGGTGGAGAGCTTTGGCAGCTACAACCCG 319

QY 1019 CCA---GGAGCAACCCCTAAGGGGACCATCTGTTGATGGAGGACATATGATATCTAC 1075
Db 318 TCGTCGGGGCCGCCAACACCGGGGGTCTTACCTCGGACGCGACCATCGACATCTGT 259

QY 1076 GAGACTCTTAGAGTCAATCAACCCCTCCATTAAAGGGATTGCCATTTAAACAATATTGG 1135
Db 258 GTCAGCACCCCGCTACAACAGCCCTCCATCGAGCGCACCAAGACCTTTCAGCAGTTCTGG 199

QY 1136 AGTGTTCGAAGTCGAACGACAGAGTGCGGACGATTTCTGTGAGCAACCACTTTAGAGCG 1195
Db 198 TCGGTGCGCCGCAACAAGCGCGCACGCGCACCGTCACTTTGGCCAAACCAAGTCAACGCC 139

QY 1196 TGGGAAAACTTAGGGATGAA 1215
Db 138 TGGCGCAACGCGGCGCTCAA 119

Search completed: November 11, 2004, 01:16:52
Job time : 6561.71 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 10, 2004, 15:57:32 ; Search time 894.922 Seconds
(without alignments)
9775.823 Million cell updates/sec

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Perfect score: 185
Sequence: 1 TCATGTAACCTCCCTTGATC.....AAAAGAGAGGATGGA 185

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Gapop 10.0 , Gapext 1.0
Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_cm.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	184	99.5	185	6	A42278 Sequence 28
2	184	99.5	185	6	A48247 Sequence 26
3	184	99.5	185	6	AR127043 Sequence
4	184	99.5	185	6	AR193071 Sequence
5	184	99.5	185	6	AR220047 Sequence
6	184	99.5	185	6	AR221330 Sequence
7	184	99.5	1022	6	A42251 Sequence 1
8	184	99.5	1022	6	A42285 Sequence 35
9	184	99.5	1022	6	AR127019 Sequence
10	184	99.5	1022	6	AR127049 Sequence
11	184	99.5	1022	6	AR220023 Sequence
12	184	99.5	1022	6	AR220053 Sequence
13	184	99.5	1022	6	AR221306 Sequence
14	184	99.5	1022	6	AR221336 Sequence
15	77.2	41.7	1789	1	AF326785 Bacillus
16	39.8	21.5	176689	5	BX000477 Zebrafish
17	38.6	20.9	158951	9	AL355390 Human DNA
18	37.6	20.3	178560	10	AC134839 Mus muscu
19	37.6	20.3	208557	10	AC125406 Mus muscu

C	20	37.4	20.2	207337	2	BX324185	BX324185 Danio rer
	21	37.2	20.1	105587	9	CNS01DU6	AL133166 Human chr
	22	37	20.0	108566	2	AC098193_6	Continuation (7 of
	23	37	20.0	110000	2	AC098192_1	Continuation (2 of
	24	37	20.0	110000	2	AC098192_2	Continuation (3 of
	25	37	20.0	120255	9	AL589167	AL589167 Human DNA
	26	37	20.0	244759	2	AC098158	AC098158 Rattus no
	27	37	20.0	253645	2	AC137382	CR383671 Danio rer
	28	36.2	19.6	127249	2	CR383671	AC105716 Rattus no
	29	36	19.5	215357	2	AC105716	AC11688 Rattus no
	30	36	19.5	231967	2	AC11688	I66494 Sequence 14
	31	35.8	19.4	7218	6	I66494	AC136569 Rattus no
	32	35.6	19.2	233510	2	AC136569	AC097745 Rattus no
	33	35.6	19.2	238007	10	AC097745	AC117880 Rattus no
	34	35.6	19.2	246818	2	AC117880	AL115455 Botrytis
	35	35.4	19.1	276	8	CNS01CFB	AL116777 Botrytis
	36	35.4	19.1	420	8	CNS01DGI	AL116140 Botrytis
	37	35.4	19.1	540	8	CNS01AIJ	AL112367 Botrytis
	38	35.4	19.1	600	8	CNS01CYC	AL450308 Homo sapi
	39	35.4	19.1	97101	2	AL450308	AL450063 Human DNA
	40	35.4	19.1	130878	9	AL450063	AC137480 Rattus no
	41	35.4	19.1	182862	2	AC125593	AC125593 Rattus no
	42	35.4	19.1	200446	2	AC125593	BX936384 Danio rer
	43	35.2	19.0	206981	2	BX936384	BX942821 Danio rer
	44	35.2	19.0	287360	2	BX942821	AC005345 Homo sapi
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ALIGNMENTS

RESULT 1
A42278
LOCUS A42278
DEFINITION Sequence 28 from Patent EP0634490.
ACCESSION A42278
VERSION A42278.1 GI:2297766
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 185)
AUTHORS De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.
TITLE Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
JOURNAL Patent: EP 0634490-A 28 18-JAN-1995;
COMMENT SOLVAY (BE)
Other publication NZ 260989 950828
Other publication BR 9402834 950613
Other publication JP 7067637 950314
Other publication FI 943389 950116
Other publication CA 2128050 950116
Other publication AU 942652 950116
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2e-45;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCATGTAACCTCCCTTGATCTATTTCATTTGTTATCAAGGATTTATACAAACAAGAGA 60
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Qy 61 CATCCATGCCGGGTTAAAGCAGTATCGTTCATCTAAACAGAGAGGNCCTGCATGAAAGGA 120

Db 61 CATCCATGCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAGGA 120
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 Db 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAACATACGGATGAAAAAAGGAGAGGAT 180
 Qy 181 GGAAA 185
 Db 181 GGAAA 185

RESULT 2
 A48247
 LOCUS A48247 185 bp DNA linear PAT 07-MAR-1997
 DEFINITION Sequence 26 from Patent EP0698667.
 ACCESSION A48247
 VERSION A48247.1 GI:2302095
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 185)
 AUTHORS De, B. E., Lahaye, A., Ledoux, P. and Detroz, R.
 TITLE Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
 JOURNAL Patent: EP 0698667-A 26 28-FEB-1996;
 SOLVAY (BE)
 COMMENT Other publication BE 1008751 960702
 Other publication BE 1008570 960604
 Other publication BR 9503454 960305
 Other publication JP 8092284 960409
 Other publication FI 953578 960127
 Other publication CA 2154628 960127
 Other publication AU 2508695 960208.

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ORIGIN

Query Match 99.5%; Score 184; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 2.2e-45;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 CATCCATGCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAGGA 120
 Qy 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAACATACGGATGAAAAAAGGAGAGGAT 180
 Db 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAACATACGGATGAAAAAAGGAGAGGAT 180
 Qy 181 GGAAA 185
 Db 181 GGAAA 185

RESULT 3
 AR127043
 LOCUS AR127043 185 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 28 from patent US 6180382.
 ACCESSION AR127043
 VERSION AR127043.1 GI:14113636
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 185)
 AUTHORS De Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
 TITLE Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
 JOURNAL Patent: US 6180382-A 28 30-JAN-2001;
 FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.5%; Score 184; DB 6; Length 185;
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 Qy 61 CATCCATGCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAGGA 120
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 Qy 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAACATACGGATGAAAAAAGGAGAGGAT 180
 Db 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAACATACGGATGAAAAAAGGAGAGGAT 180
 Qy 181 GGAAA 185
 Db 181 GGAAA 185

RESULT 4
 AR193071
 LOCUS AR193071 185 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 26 from patent US 6346407.
 ACCESSION AR193071
 VERSION AR193071.1 GI:20239036
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 185)
 AUTHORS De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
 TITLE Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
 JOURNAL Patent: US 6346407-A 26 12-FEB-2002;
 FEATURES Location/Qualifiers
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 1..185
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 99.5%; Score 184; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 2.2e-45;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATGTAACCTCGCCTTGATCTATTTTCATCTTAAAGAGATTATACAAAGGATTTATACAAACAAAGGA 60
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 Db 61 CATCCATGCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAGGA 120
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 Qy 181 GGAAA 185
 Db 181 GGAAA 185

Db 181 GGAAA 185

RESULT 5
AR220047
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

ORIGIN

Query Match
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Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CATCCATGCCGGGTTAAAGCAGTAGTTCGTTCCATCTTAACAGAGAGGNCCTGCATGAAGGA 120
DB 61 CATCCATGCCGGGTTAAAGCAGTAGTTCGTTCCATCTTAACAGAGAGGNCCTGCATGAAGGA 120

QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAAATACGGATGAAAAAGGAGAGGGAT 180
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QY 181 GGAAA 185
DB 181 GGAAA 185

RESULT 6
AR221330
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

ORIGIN

Query Match
Best Local Similarity 99.5%; Score 184; DB 6; Length 185;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CATCCATGCCGGGTTAAAGCAGTAGTTCGTTCCATCTTAACAGAGAGGNCCTGCATGAAGGA 120
DB 61 CATCCATGCCGGGTTAAAGCAGTAGTTCGTTCCATCTTAACAGAGAGGNCCTGCATGAAGGA 120

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QY 181 GGAAA 185
DB 181 GGAAA 185

RESULT 7
AR2251
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

ORIGIN

Query Match
Best Local Similarity 99.5%; Score 184; DB 6; Length 1022;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACCTCGCCTTGATCTATTTCATTTGTTATCAAAAGGATTTTATACAAACAAGAGA 60
DB 1 TCATGTAACCTCGCCTTGATCTATTTCATTTGTTATCAAAAGGATTTTATACAAACAAGAGA 60

QY 61 CATCCATGCCGGGTTAAAGCAGTAGTTCGTTCCATCTTAACAGAGAGGNCCTGCATGAAGGA 120
DB 61 CATCCATGCCGGGTTAAAGCAGTAGTTCGTTCCATCTTAACAGAGAGGNCCTGCATGAAGGA 120

QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAAATACGGATGAAAAAGGAGAGGGAT 180
DB 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAAATACGGATGAAAAAGGAGAGGGAT 180

QY 181 GGAAA 185
DB 181 GGAAA 185

QY 1 TCATGTAACCTCGCCTTGATCTATTTCATTTGTTATCAAAAGGATTTTATACAAACAAGAGA 60
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QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAAATACGGATGAAAAAGGAGAGGGAT 180
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QY 181 GGAAA 185
DB 181 GGAAA 185

RESULT 7
A42251
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

ORIGIN

Query Match
Best Local Similarity 99.5%; Score 184; DB 6; Length 1022;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACCTCGCCTTGATCTATTTCATTTGTTATCAAAAGGATTTTATACAAACAAGAGA 60
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QY 61 CATCCATGCCGGGTTAAAGCAGTAGTTCGTTCCATCTTAACAGAGAGGNCCTGCATGAAGGA 120
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QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAAATACGGATGAAAAAGGAGAGGGAT 180
DB 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAAATACGGATGAAAAAGGAGAGGGAT 180

QY 181 GGAAA 185
DB 181 GGAAA 185

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LOCUS           Sequence 35 from Patent EP0634490.
DEFINITION      A42285
ACCESSION       A42285
VERSION         A42285.1 GI:2297772
KEYWORDS        unidentified
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 1022)
AUTHORS        De, B.E., Lahaya, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and
                Vetter, R.
TITLE          xylanase derived from a bacillus species, expression vectors for
                such xylanase and other proteins, host organisms therefor and use
                thereof
JOURNAL        Patent: EP 0634490-A 35 18-JAN-1995;
COMMENT        SOLVAY (BE)
                Other publication NZ 260989 950828
                Other publication BR 9402834 950613
                Other publication JP 7057637 950314
                Other publication FI 943389 950116
                Other publication CA 2128050 950116
                Other publication NO 942652 950116
                Other publication AU 6743294 950127
                Other publication GB 2279955 950118.
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Query Match      99.5%; Score 184; DB 6; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
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DB      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
QY      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
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DB      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
QY      181 GGAAA 185
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DB      181 GGAAA 185

RESULT 9
AR127019        AR127019        1022 bp      DNA      linear      PAT 16-MAY-2001
LOCUS           Sequence 1 from patent US 6180382.
DEFINITION      AR127019
ACCESSION       AR127019
VERSION         AR127019.1 GI:14113612
KEYWORDS        Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 1022)
AUTHORS        De Buy, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and
                Vetter, R.
TITLE          xylanase derived from a bacillus species, expression vectors for
                such xylanase and other proteins, host organisms therefor and use
                thereof
JOURNAL        Patent: US 6180382-A 1 30-JAN-2001;
FEATURES       source
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Query Match      99.5%; Score 184; DB 6; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
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DB      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
QY      181 GGAAA 185
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DB      181 GGAAA 185

RESULT 10
AR127049        AR127049        1022 bp      DNA      linear      PAT 16-MAY-2001
LOCUS           Sequence 35 from patent US 6180382.
DEFINITION      AR127049
ACCESSION       AR127049
VERSION         AR127049.1 GI:14113642
KEYWORDS        Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 1022)
AUTHORS        De Buy, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and
                Vetter, R.
TITLE          xylanase derived from a bacillus species, expression vectors for
                such xylanase and other proteins, host organisms therefor and use
                thereof
JOURNAL        Patent: US 6180382-A 35 30-JAN-2001;
FEATURES       source
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Query Match      99.5%; Score 184; DB 6; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
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DB      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
QY      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
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DB      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
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DB      181 GGAAA 185

RESULT 11
AR220023        AR220023        1022 bp      DNA      linear      PAT 26-SEP-2002
LOCUS           Sequence 1 from patent US 6423523.
DEFINITION      AR220023
ACCESSION       AR220023
VERSION         AR220023.1 GI:14113612
KEYWORDS        Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 1022)
AUTHORS        De Buy, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and
                Vetter, R.
TITLE          xylanase derived from a bacillus species, expression vectors for
                such xylanase and other proteins, host organisms therefor and use
                thereof
JOURNAL        Patent: US 6180382-A 1 30-JAN-2001;
FEATURES       source
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Query Match      99.5%; Score 184; DB 6; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TCATGTAACTCGCCCTTGATCTATTTTCATTTGTATCAAAAGGATTTATACACAAACAAGAGA 60
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QY      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
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DB      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
QY      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
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Best Local Similarity 100.0%; Pred. No. 1.9e-45;
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DB      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
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DB      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
QY      181 GGAAA 185
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DB      181 GGAAA 185

RESULT 10
AR127049        AR127049        1022 bp      DNA      linear      PAT 16-MAY-2001
LOCUS           Sequence 35 from patent US 6180382.
DEFINITION      AR127049
ACCESSION       AR127049
VERSION         AR127049.1 GI:14113642
KEYWORDS        Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 1022)
AUTHORS        De Buy, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and
                Vetter, R.
TITLE          xylanase derived from a bacillus species, expression vectors for
                such xylanase and other proteins, host organisms therefor and use
                thereof
JOURNAL        Patent: US 6180382-A 35 30-JAN-2001;
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Query Match      99.5%; Score 184; DB 6; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 TCATGTAACTCGCCCTTGATCTATTTTCATTTGTATCAAAAGGATTTATACACAAACAAGAGA 60
QY      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
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DB      61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGCTGCATGAAGAAGA 120
QY      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
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DB      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
QY      181 GGAAA 185
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DB      181 GGAAA 185

RESULT 11
AR220023        AR220023        1022 bp      DNA      linear      PAT 26-SEP-2002
LOCUS           Sequence 1 from patent US 6423523.
DEFINITION      AR220023
ACCESSION       AR220023
VERSION         AR220023.1 GI:14113612
KEYWORDS        Unknown.
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 1022)
AUTHORS        De Buy, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and
                Vetter, R.
TITLE          xylanase derived from a bacillus species, expression vectors for
                such xylanase and other proteins, host organisms therefor and use
                thereof
JOURNAL        Patent: US 6180382-A 1 30-JAN-2001;
FEATURES       source
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ORIGIN
Query Match      99.5%; Score 184; DB 6; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
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QY      1 TCATGTAACTCGCCCTTGATCTATTTTCATTTGTATCAAAAGGATTTATACACAAACAAGAGA 60
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QY      121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACCGATGAAAAAAGGAGGGAT 180
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ACCESSION AR220023
 VERSION AR220023.1 GI:23324441
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1022)
 AUTHORS de Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
 TITLE Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
 JOURNAL Patent: US 6423523-A 1 23-JUL-2002;
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 Best Local Similarity 100.0%; Pred. No. 1.9e-45;
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 QY 1 TCATGTAACCTCGCTTGATCTATTTTCATTTGTATCAAGGATTTATACAAACAAGAGA 60
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 QY 61 CATCCATGCGGGTTAAAGCAGTATCGTTCATCTTAACAGAGAAGNCTGCATGAAGGA 120
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 QY 181 GGAAA 185
 Db 181 GGAAA 185
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 AR220053
 LOCUS AR220053 1022 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 35 from patent US 6423523.
 ACCESSION AR220053
 VERSION AR220053.1 GI:23324471
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1022)
 AUTHORS de Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
 TITLE Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
 JOURNAL Patent: US 6423523-A 35 23-JUL-2002;
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 Db 1 TCATGTAACCTCGCTTGATCTATTTTCATTTGTATCAAGGATTTATACAAACAAGAGA 60
 QY 61 CATCCATGCGGGTTAAAGCAGTATCGTTCATCTTAACAGAGAAGNCTGCATGAAGGA 120
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 QY 181 GGAAA 185
 Db 181 GGAAA 185
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 AR221336
 LOCUS AR221336 1022 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 35 from patent US 6426211.
 ACCESSION AR221336
 VERSION AR221336.1 GI:23328311
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1022)
 AUTHORS de Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
 TITLE Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
 JOURNAL Patent: US 6426211-A 35 30-JUL-2002;
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 DEFINITION Sequence 1 from patent US 6426211.
 ACCESSION AR221306
 VERSION AR221306.1 GI:23328281
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
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 AUTHORS de Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
 TITLE Xylanase derived from a Bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
 JOURNAL Patent: US 6426211-A 1 30-JUL-2002;
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 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ACCESSION AR221336
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 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1022)
 AUTHORS de Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
 TITLE Xylanase derived from a Bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
 JOURNAL Patent: US 6426211-A 35 30-JUL-2002;
 FEATURES
 source Location/Qualifiers

```

Qy 76 AAAGCAGTATCGTTCCATCTCTAACAGAGAGNCNCTGCATGAAACGAGAGGTGATGGGTT--TT 133
    |||||
Db 454 AGCAGAGTATCGAT--AATCTAATAGTAGTGGGGCATGAAAGGAGGTGATGAATTCGTT 511
    |||||

Qy 134 TCATCTTAGGGATGACAGACAACAAATACGGATCAAAAAAGGAGAGGGATGGAA 184
    |||||
Db 512 TCATCTTAGAGATGACAGAAATCAAAGGATG-AAAAAGGAGAGAGAAATGGAA 561
    |||||

Search completed: November 10, 2004, 21:26:34
Job time : 897.922 secs

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Search completed: November 10, 2004, 21:26:34
Job time : 897.922 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 15:55:17 : Search time 117.352 Seconds
(without alignments)
8275.436 Million cell updates/sec

Title: US-09-909-207-26
Perfect score: 185
Sequence: 1 TCATGTAACCTGCCTTGATC.....AAAAGGAGAGGATGGAAA 185

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 23Sep04: *
1: geneseqn1980a: *
2: geneseqn1990a: *
3: geneseqn2000a: *
4: geneseqn2001a: *
5: geneseqn2001bs: *
6: geneseqn2002a: *
7: geneseqn2002bs: *
8: geneseqn2003a: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004a: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	184	99.5	1022	2	Aaq80923 B. pumilu
2	183	98.9	184	2	Aaq73996 Xylanase
3	32.2	17.4	23439	2	Aav74349 Staphyloc
4	32	17.3	405	8	Abx38967 Bovine ES
5	31.6	17.1	302	3	Aaa41613 Human sec
6	31.6	17.1	28149	5	Abal7961 Human ner
7	31.6	17.1	32192	5	Abal7963 Human ner
8	31.6	17.1	110000	12	Continuation (5 of
9	31.6	17.1	110000	12	Continuation (6 of
10	31.4	17.0	110000	2	Continuation (5 of
11	31.2	16.9	443	4	Aai91410 Human pol
12	31	16.8	390	6	Abk39185 cDNA enco
13	31	16.8	390	8	Acail1514 Human lun
14	31	16.8	390	8	Acac2700 Lung can
15	31	16.8	390	10	Adh46742 Human lun
16	31	16.8	410	5	Abv39054 Human pro
17	31	16.8	2262	10	Adf00565 Bacterial
18	31	16.8	5124	4	Aak75882 Human imm
19	31	16.8	32183	4	Aas35994 Human car
20	31	16.8	32183	10	Ade46688 Human car
21	31	16.8	51935	4	Aak75883 Human imm

C	22	30.8	16.6	1132	6	ABZ15647
	23	30.8	16.6	262090	12	ADQ59207
	24	30.6	16.5	1238	5	AAS68017
	25	30.2	16.3	930	8	ACA28595
	26	30	16.2	831	10	ACA55420
	27	30	16.2	831	12	ADI55216
	28	30	16.2	15962	6	ABA01445
C	29	30	16.2	43795	3	AZ292583
C	30	29.8	16.1	6718	4	ABL09262
C	31	29.8	16.1	9147	4	ABL09206
C	32	29.8	16.1	178896	6	ABQ88146
	33	29.6	16.0	553	3	ACA44275
	34	29.6	16.0	610	9	ACH04273
	35	29.6	16.0	977	5	AAK91468
	36	29.6	16.0	977	5	AAAS40051
	37	29.6	16.0	977	9	ADB33011
	38	29.6	16.0	1143	5	AAH65014
	39	29.6	16.0	1323	8	ACA01823
	40	29.6	16.0	1761	6	AAI47164
	41	29.6	16.0	4436	4	ABL07432
C	42	29.6	16.0	5669	6	ABA01094
	43	29.6	16.0	8924	4	ABL07438
	44	29.6	16.0	110000	6	ABX08336
	45	29.6	16.0	110000	12	ADJ25985

ALIGNMENTS

RESULT 1
AAQ80923
ID AAQ80923 standard; DNA; 1022 BP.

AC AAQ80923;

DT 02-AUG-1995 (first entry)

DE B. pumilus xylanase gene.

KW Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping; biobleaching;
bleaching; Bacillus licheniformis; ss.

OS Bacillus pumilus.

EH Key Location/Qualifiers
FT 5'UTR 1..185
FT /tag= a
FT /note= "claim 12"

FT misc_difference 107
FT /tag= b
FT /note= "base n at position 107 is not identified in the specification"

FT CDS 186..869
FT /tag= c
FT sig_peptide 186..266
FT /tag= d
FT /note= "claim 11"

FT mat_peptide 267..866
FT /tag= e
FT /EC_number= "3.2.1.8"

FT /note= "claim 10"

XX GB2279955-A.

XX 18-JAN-1995.

PD 15-JUL-1993; 93GB-00014780.

PF 15-JUL-1993; 93GB-00014780.

PR (SOLV) SOLVAY & CIE.

PA Amory A, Andre C, De Buyl E, Detroz R, Lahaye A, Ledoux P;

XX

PI

XX WPI: 1995-039214/06.
 DR P-PSDB; AAR68849.
 XX
 PT Purified xylanase from *Bacillus pumilus* PRL B12 - esp. produced in
 PT transformed *Bacillus licheniformis*, and related DNA, vectors, etc., used
 PT for pre-treatment of wood pulp to reduce chlorine or ozone consumption in
 PT subsequent bleaching.
 XX Claim 13; Fig 1a-1b; 97pp; English.
 XX
 CC A *Bacillus pumilus* PRL B12 (ATCC 55443) gene library was screened for
 CC recombinant plasmids carrying the xylanase gene. A chromosomal fragment
 CC obtained from isolate pBPX1 was subcloned and expressed in *Escherichia*
 CC coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3AI
 CC fragment) carried by a selected transformant is given in AAQ80923
 XX
 SQ Sequence 1022 BP; 329 A; 197 C; 229 G; 266 T; 0 U; 1 Other;
 Query Match 99.5%; Score 184; DB 2; Length 1022;
 Best Local Similarity 100.0%; Pred. No. 6.7e-49; Mismatches 0; Indels 0; Gaps 0;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCATGTAACCTCGCTTGATCTATTTCATTTGTATCAAAAGGATTATACACAAACAAGAGA 60
 DB 1 TCATGTAACCTCGCTTGATCTATTTCATTTGTATCAAAAGGATTATACACAAACAAGAGA 60
 QY 61 CATCATGCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGNCATGATGAAGGA 120
 DB 61 CATCATGCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGNCATGATGAAGGA 120
 QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAGGAGGGAT 180
 DB 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAGGAGGGAT 180
 QY 181 GGAAA 185
 DB 181 GGAAA 185
 RESULT 2
 ID AAQ73996 standard; DNA; 184 BP.
 XX
 AC AAQ73996;
 XX
 DT 16-OCT-2003 (revised)
 DT 15-MAY-1996 (first entry)
 XX
 DE Xylanase promoter.
 XX
 KW Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
 KW promoter; ss.
 XX
 OS *Bacillus pumilus*; strain PRL B12 (ATCC 55443).
 XX
 PN AU9525086-A.
 XX
 PD 08-FEB-1996.
 XX
 PF 19-JUL-1995; 95AU-00025086.
 XX
 PR 26-JUL-1994; 94BE-00000706.
 PR 17-MAY-1995; 95BE-00000448.
 XX
 PA (SOLV) SOLVAY SA.
 XX
 PI De Buyl E, Lahaye A, Ledoux P, Detroz R;
 XX
 DR WPI: 1996-117341/13.
 XX
 PT *Bacillus* derived xylanase active over wide pH range - used in treatment
 PT of paper pulp, animal feeds and in bakery goods.

XX Claim 26; Page 69; 94pp; English.
 XX
 CC The *Bacillus pumilus* PRL B12 xylanase gene promoter (AAQ73996) and
 CC presequence (AAQ73997) were incorporated into vectors used for the
 CC expression of DNA (see AAT16101) coding for a mature, thermostable
 CC xylanase (AAR92053) of *Bacillus* sp. 720/1. The enzyme can be produced in
 CC transformed hosts, pref. *Bacillus licheniformis* or *B. pumilus*, for use in
 CC the paper-pulp, animal feed and baking industries. (Updated on 16-OCT-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 184 BP; 63 A; 29 C; 45 G; 46 T; 0 U; 1 Other;
 Query Match 98.9%; Score 183; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.9e-49; Mismatches 0; Indels 0; Gaps 0;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCATGTAACCTCGCTTGATCTATTTCATTTGTATCAAAAGGATTATACACAAACAAGAGA 60
 DB 1 TCATGTAACCTCGCTTGATCTATTTCATTTGTATCAAAAGGATTATACACAAACAAGAGA 60
 QY 61 CATCATGCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGNCATGATGAAGGA 120
 DB 61 CATCATGCCGGGTTAAAGCAGTATCGTTCCATCTTAACAGAGAAGGNCATGATGAAGGA 120
 QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAGGAGGGAT 180
 DB 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAGGAGGGAT 180
 QY 181 GGAA 184
 DB 181 GGAA 184
 RESULT 3
 ID AAV74349 standard; DNA; 23439 BP.
 XX
 AC AAV74349;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE *Staphylococcus aureus* contig SEQ ID #38.
 XX
 KW Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS *Staphylococcus aureus*.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 481..540
 FT /*tag= a
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They are
 FT included to maintain the nucleotide numbering given in
 FT the specification for this DNA sequence"
 FT 2281..2340
 FT misc_feature /*tag= b
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They are
 FT included to maintain the nucleotide numbering given in
 FT the specification for this DNA sequence"
 FT 4081..4140
 FT misc_feature /*tag= c
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They are
 FT included to maintain the nucleotide numbering given in
 FT the specification for this DNA sequence"
 FT 5881..5940
 FT misc_feature /*tag= d
 FT /note= "these bases represent a line of missing text in

the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

7681. .7740

/*tag= e

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

9481. .9540

/*tag= f

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

11281. .11340

/*tag= g

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

13081. .13140

/*tag= h

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

14881. .14940

/*tag= i

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

16681. .16740

/*tag= j

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

18481. .18540

/*tag= k

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

20281. .20340

/*tag= l

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

22081. .22140

/*tag= m

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

BP786519-A2.

30-JUL-1997.

07-JAN-1997; 97EP-00100117.

05-JAN-1996; 96US-0009861P.

(HUMA-) HUMAN GENOME SCI INC.

Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA; WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus -

stored on computer readable medium and used in the production of anti-S. aureus vaccines.

Claim 1; Page 339-352; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S. aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer readable medium

Sequence 23439 BP; 7768 A; 3506 C; 4455 G; 6921 T; 0 U; 789 Other;

Query Match 17.4%; Score 32.2; DB 2; Length 23439;

Best Local Similarity 52.2%; Pred. No. 14;

Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

44 TATACACAAACAGAGACATCCATCCCGGGTTTAAAGCAGATATCGTTCCATCTAACAGAGA 103

11481 TATGTATATAACCGTGTGATGGACTTAGGCGTTCATTGTTTCAGTCGTTGGTGGGATAAC 11540

104 AGCNCTGCATGAAGAGAGGTGATGGGTTTTTCATCTTAGGATGACAGACATACCGAT 163

11541 ACGACCAAAAGAAATTTACGAAACGTTTGTTCATTAATATGSAAGATTAATGATAACGAT 11600

164 GAAAAAAGGAGAGG 177

11601 AAAAAACGAGATG 11614

RESULT 4

ABX38967/c

ID ABX38967 standard; cDNA; 405 BP.

XX ABX38967;

AC AC

XX XX

DT 20-FEB-2003 (first entry)

XX XX

DE Bovine EST associated with lactation/muscle/fat deposition #4132.

XX XX

KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;

KW muscle deposition; fat deposition; genome mapping; gene identification;

KW gene analysis; cattle breeding.

XX XX

OS Bos Taurus.

XX XX

PN US2002137139-A1.

XX XX

PD 26-SEP-2002.

XX XX

PF 24-SEP-2001; 2001US-00960352.

XX XX

PR 12-JAN-1999; 99US-0115707P.

PR 11-JAN-2000; 2000US-00480902.

XX XX

PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

XX XX

PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX
 PS Claim 2: SEQ ID NO 4132; 245pp; English.
 XX
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non-translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 405 BP; 138 A; 63 C; 64 G; 139 T; 0 U; 1 Other;
 Query Match 17.3%; Score 32; DB 8; Length 405;
 Best Local Similarity 53.7%; Pred. No. 4.1;
 Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 OY 21 TATTTCATTGTCATCAAGGATTTATACAAACAGAGACATCCATCGGGTTAAAGC 80
 Db 122 TATTTCATTGTCATCAAGGATTTATACAAAGTTTACTACGAAATCTGCTTCAACATGA 63
 OY 81 AGTATCGTTCATCTACAGAGAGGNCCTGCATGAAAGAGGTGATGGTTTTCATCTT 140
 Db 62 AGCAATTTCTCTTCAAGATATACACCTGCATGGAAGAGTGATTCCTTTACATTTA 3
 OY 141 A 141
 Db 2 A 2
 RESULT 5
 AAA41613/c
 ID AAA41613 standard; cDNA; 302 BP.
 XX
 AC AAA41613;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE Human secreted expressed sequence tag SEQ ID NO:353.
 XX
 KW Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
 KW expressed sequence tag; EST; probe; chemotactic; proliferative;
 KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
 KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
 KW antiviral; antidiabetic; antiaesthatic; vulnerary; antiparkinsonian;
 KW antitumor; osteoprotective; neuroprotective; nootropic; antipsoriatic;
 KW cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
 KW
 KW autoimmune disorder; multiple sclerosis; allergic condition; insulin
 KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
 KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
 KW central nervous system disorder; Alzheimer's disease; stroke;
 KW Parkinson's disease; Huntington's disease; coagulation disorder;
 KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
 KW infection; depression; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO2000021990-A1.
 XX
 PD 20-APR-2000.
 XX
 PF 15-OCT-1999; 99WO-US024205.
 XX
 PR 15-OCT-1998; 98US-0104435P.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merzberg D, Treacy M;
 XX WPI; 2000-317937/27.
 XX
 DR Isolated polynucleotides, and encoded proteins, comprising secreted
 PT expressed sequence tags (sESTs), useful for treating various disorders
 PT such as autoimmune, infectious, and central nervous system disorders.
 XX
 Claim 1; Page 249; 618pp; English.
 AA441261 to AAA43419 represent specifically claimed secreted expressed
 CC sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue
 CC sources. The sESTs can have a range of activities depending on the
 CC tissues they were isolated from. The activities include: chemotactic;
 CC proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
 CC haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial;
 CC antifungal; antiviral; antidiabetic; antiaesthatic; vulnerary; antitumor;
 CC osteoprotective; neuroprotective; nootropic; antiparkinsonian; antipsoriatic;
 CC cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be
 CC used for gene therapy and in vaccines. The sESTs are useful as probes for
 CC the identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the sESTs. Proteins encoded by the sESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA43420 to AAA43425 represent linker variants which are given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 302 BP; 67 A; 84 C; 62 G; 89 T; 0 U; 0 Other;
 Query Match 17.1%; Score 31.6; DB 3; Length 302;
 Best Local Similarity 53.8%; Pred. No. 5;
 Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 OY 56 AGAGACATCCATCGCGGGTTAAAGCAGTATGTTCCATCTTAACAGAGAGGNCCTGATGA 115
 Db 180 AGAGGTTTAAATGGGCTCAAAAAAGTGGCTGCTCCACAGAGAAAAAGCTCTAAA 121
 OY 116 AAGGAGGTGATGGGTTTTCATCTTAGGATGACAGAACATACGGATGAAAAAGGAG 174
 Db 120 TAGAACCTGGCAGGAAATACATTTTAAGAGTTGGGAGAGAGTAAACCATAGTAAGAGGAG 62
 RESULT 6
 ABA17961/c
 ID ABA17961 standard; DNA; 28149 BP.
 XX

AC ABA17961;
XX 23-JAN-2002 (first entry)
XX Human nervous system related polynucleotide SEQ ID NO 10292.
DE
DE
XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiskinking; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
XX 16-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US001334.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0242221P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
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PR 08-NOV-2000; 2000US-0246533P.
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PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
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PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.

PR 25-SEP-2000; 2000US-0234997P.
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 PR 29-SEP-2000; 2000US-0236370P.
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 PR 20-OCT-2000; 2000US-0242221P.
 PR 01-NOV-2000; 2000US-0246179P.
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 PR 08-NOV-2000; 2000US-0246475P.
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 PR 08-NOV-2000; 2000US-0246523P.
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 PR 08-NOV-2000; 2000US-0246613P.
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 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
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 PR 01-DEC-2000; 2000US-0250331P.
 PR 01-DEC-2000; 2000US-0251160P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.

PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-541565/60.
 XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 XX Disclosure; SEQ ID NO 10294; 1701pp + Sequence Listing; English.
 XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 32192 BP; 7965 A; 7802 C; 8055 G; 8370 T; 0 U; 0 Other;

Query Match 17.1%; Score 31.6; DB 5; Length 32192;
 Best Local Similarity 53.8%; Pred. No. 24; Mismatches 55; Indels 0; Gaps 0;
 Matches 64; Conservative 0;
 QY 56 AGAGACATCCATCGCCGGTTAAAGCAGATATCGTTCCATCTAACAGAGAGAGNCTGCATGA 115
 Db 14550 AGAGGTTTAAATGGGCTCAAAAAGTGGCTGCTCTCCACAGAGAAAGCTCTAAAA 14491
 QY 116 AAGGAGGTGATGGGTTTTTCATCTTAGGATGACAGAAACATACGGATGAAAAAGAG 174
 Db 14490 TAGACGTGGCAGGAATACATTAAAGTGGGAGAGAGTAACACAGATAAGAGGAG 14432

RESULT 8
 ADH69807_4/c
 Continuation (5 of 7) of ADH69807 from base 400001 (Human Vbeta gene.)
 WP Sequence split into 7 fragments LOCUS ADH69807 Accession Adh69807
 WP Fragment Name Begin End
 WP ADH69807_0 1 110000
 WP ADH69807_1 100001 210000
 WP ADH69807_2 200001 310000
 WP ADH69807_3 300001 410000
 WP ADH69807_4 400001 510000
 WP ADH69807_5 500001 610000
 WP ADH69807_6 600001 684973

Query Match 17.1%; Score 31.6; DB 12; Length 110000;
 Best Local Similarity 49.1%; Pred. No. 36; Mismatches 85; Indels 0; Gaps 0;
 Matches 82; Conservative 0;
 QY 19 TCTATTTTCATTGTATCAAGGATTTATACACAAACAGAGACATCATCCCGGTTAAA 78
 Db 104161 TCCATTGCAACTGTTTGTAAAGCTATGAACATATAAATACATAGCTTTGAGTGCCTGTA 104102
 QY 79 GCAGTATCGTTCCATCTAACAGAGAGAGNCTGATGAAGAGAGGTGATGGTGTTCATC 138
 Db 104101 ATAGCAAGATTTTACCTAATTAAGAGGTTGGGAAGGAGAGTGGCATTTGAGTTGGTTC 104042
 QY 139 TTAGGGATGACAGACAATACCGGATGAAAAAGGAGGAGGATGAAA 185

Db 104041 TGAAGGATGACAGGAGTGAAGTCTGCAACCCAGAGAGAGAACCA 103995

RESULT 9

ADH69807_5/c
Continuation (6 of 7) of ADH69807 from base 500001 (Human Vbeta gene.)

WP Sequence split into 7 fragments LOCUS ADH69807 Accession Adh69807
Fragment Name Begin End
WP ADH69807_0 1 110000
WP ADH69807_1 100001 210000
WP ADH69807_2 200001 310000
WP ADH69807_3 300001 410000
WP ADH69807_4 400001 510000
WP ADH69807_5 500001 610000
WP ADH69807_6 600001 684973

Query Match 17.1%; Score 31.6; DB 12; Length 110000;
Best Local Similarity 49.1%; Pred. No. 36;
Matches 82; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 19 TCTATTTTCATTTGTATCAAGAGTTTATACAAACAGAGACATCCATCCCGGGTTAAA 78
DB 4161 TCCATGTCAACTGTTTGTAAAGCTATGAACATAAAACTACATAGCTTTGAGTGCCTGTA 4102
QY 79 GCAGTATCGTTCATCTACAGAGAGGCTCATGAAAGGAGGTGATGGGTTTTCATC 138
DB 4101 ATAGCAGATTTTACCTAATTAAGAGTTGGAAAGGAGTGGCATTTGAGTTGGTTTC 4042
QY 139 TTAGGATGACAGAAACATACGATGAAAGGAGGAGGATGGA 185
DB 4041 TGAAGGATGACAGGAGTGAAGTCTGCAACCCAGAGAGAGAACCA 3995

RESULT 10

AAV21209_04
Continuation (5 of 17) of AAV21209 from base 400001 (Methanococcus jannaschii circular
WP Sequence split into 17 fragments LOCUS AAV21209 Accession Aav21209

Fragment Name Begin End
WP AAV21209_00 1 110000
WP AAV21209_01 100001 210000
WP AAV21209_02 200001 310000
WP AAV21209_03 300001 410000
WP AAV21209_04 400001 510000
WP AAV21209_05 500001 610000
WP AAV21209_06 600001 710000
WP AAV21209_07 700001 810000
WP AAV21209_08 800001 910000
WP AAV21209_09 900001 1010000
WP AAV21209_10 1000001 1110000
WP AAV21209_11 1100001 1210000
WP AAV21209_12 1200001 1310000
WP AAV21209_13 1300001 1410000
WP AAV21209_14 1400001 1510000
WP AAV21209_15 1500001 1610000
WP AAV21209_16 1600001 1664976

Query Match 17.0%; Score 31.4; DB 2; Length 110000;
Best Local Similarity 59.6%; Pred. No. 42;
Matches 53; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 17 GATCTATTTTCATTTGTATCAAGGATTTATACAAACAGAGACATCCATCCCGGGTTA 76
DB 92343 GAATCATGTGCGATTGAATCGTAGTTTATCATCATTTTAAGCTACTTACAGCCCTTCTA 92402
QY 77 AGCAGTATCTGTTTCATCTAACAGAGAAG 105
DB 92403 ATTCAATTTTTTCTTTTCAACTGAGAAG 92431

RESULT 11

AAI91410
ID AAI91410 standard; cDNA; 443 BP.

XX AAI91410;
XX AC
DT 06-NOV-2001 (first entry)
XX Human polynucleotide SEQ ID NO 11470.
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
OS Homo sapiens.
FN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX DR P-PSDB; AAO11479.
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX Claim 1; SEQ ID NO 11470; 1399pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 443 BP; 143 A; 80 C; 112 G; 108 T; 0 U; 0 Other;
Query Match 16.9%; Score 31.2; DB 4; Length 443;
Best Local Similarity 50.3%; Pred. No. 7.6;
Matches 75; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 37 AAGGATTTATACAAACAGAGACATCCATCCCGGGTTAAAGCAGTATCGTTCATCTA 96
DB 132 AAGGATAGCAAGCGCAGACAAACATAGATAATTTCTTCAAGGAGTTCAGCTCTAATG 191
QY 97 ACAGAGAAGNCTGCTGATGAAGAGGAGGTGATGGGTTTTTCATCTTAGGATGACAGAACAA 156
DB 192 GGAGGAAGACAGCAAGCAAGAGGTGAAGAGAGACAGCAAGCTAGGGCAGTGCAGAAATG 251
QY 157 TACGGATGAAAAAGGAGAGGAGGATGAAA 185
DB 252 GAGCAAGGGGAAAGAAAGGAATCGACA 280
RESULT 12
ABK39185
ID ABK39185 standard; cDNA; 390 BP.
XX AC
XX ABK39185;

CC polynucleotide is useful for isolating a full-length gene from a suitable
 CC library. The present sequence is a cDNA (full length, extended or
 CC partial) isolated from a library derived from lung tumour/cancer cells.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO at seqdata.uspto.gov/sequence.html?DocId=20020197669

XX Sequence 390 BP; 96 A; 92 C; 83 G; 119 T; 0 U; 0 Other;

Query Match 16.8%; Score 31; DB 8; Length 390;
 Best Local Similarity 48.8%; Pred. No. 8.4;
 Matches 82; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 14 CTTGATCTATTTTCATTGTATCAAGGATTATACAAAGAGATCCATCCCGGG 73
 Db 175 CATGAATCTCTGTTTCGTAGCAATGATCTCACAGTTGTCTGCTGCCACTCCGAG 234

QY 74 TTAAGCAGTATCGTTCCATCTAACAGAGAAGNCTGCATGAAAGAGAGGATG 133
 Db 235 TTTATTGGTGTGTTTCTCTTTGAGATCCATGCAATTCCTGTTGAAATCTCTCGAACTC 294

QY 134 TCATCTTAGGATGACAGACAAATACGATGAAAGAGAGGAGGATG 181

Db 295 CCTCATTAGGTATGAATAGCATGATGATTCATGATTAAGTACGGAAGG 342

RESULT 14

ACA02700
 ID ACA02700 standard; cDNA; 390 BP.

XX ACA02700;

AC ACA02700;

DT 22-MAY-2003 (first entry)

XX Lung cancer therapy and diagnosis associated cDNA #1189.

DE Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ss.

XX Homo sapiens.

XX US2002172952-A1.

PN 21-NOV-2002.

XX 10-JUL-2001; 2001US-00902941.

XX 30-JUN-1999; 99US-00346492.

PR 15-OCT-1999; 99US-00419356.

PR 17-DEC-1999; 99US-00466867.

PR 30-DEC-1999; 99US-00476300.

PR 06-MAR-2000; 2000US-00519642.

PR 22-MAR-2000; 2000US-00533077.

PR 10-APR-2000; 2000US-00546259.

PR 27-APR-2000; 2000US-00560406.

PR 05-JUN-2000; 2000US-00589184.

PR 11-JUL-2000; 2000US-00614124.

PR 29-AUG-2000; 2000US-00651563.

PR 08-SEP-2000; 2000US-00658824.

PR 26-SEP-2000; 2000US-00671325.

PR 06-OCT-2000; 2000US-00677419.

PR 30-OCT-2000; 2000US-00702705.

PR 13-DEC-2000; 2000US-00736457.

XX Example 1; SEQ ID NO 1223; 82pp; English.

XX The invention describes an isolated polynucleotide comprising one of 32
 CC sequences, complement or degenerate variants of them. The polynucleotide
 CC is useful for preparing a composition e.g. a vaccine or for gene therapy,
 CC for treating or inhibiting development of cancer, e.g. lung cancer. This
 CC sequence represents a polynucleotide associated with the compositions and
 CC methods for the therapy and diagnosis of lung cancer

XX Sequence 390 BP; 96 A; 92 C; 83 G; 119 T; 0 U; 0 Other;

Query Match 16.8%; Score 31; DB 8; Length 390;
 Best Local Similarity 48.8%; Pred. No. 8.4;
 Matches 82; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 14 CTTGATCTATTTTCATTGTATCAAGGATTATACAAAGAGATCCATCCCGGG 73
 Db 175 CATGAATCTCTGTTTCGTAGCAATGATCTCACAGTTGTCTGCTGCCACTCCGAG 234

QY 74 TTAAGCAGTATCGTTCCATCTAACAGAGAAGNCTGCATGAAAGAGGATG 133
 Db 235 TTTATTGGTGTGTTTCTCTTTGAGATCCATGCAATTCCTGTTGAAATCTCTCGAACTC 294

QY 134 TCATCTTAGGATGACAGACAAATACGATGAAAGAGAGGAGGATG 181

Db 295 CCTCATTAGGTATGAATAGCATGATGATTCATGATTAAGTACGGAAGG 342

RESULT 15

ADH46742

ID ADH46742 standard; cDNA; 390 BP.

XX ADH46742;

XX 25-MAR-2004 (first entry)

DE Human lung tumour cDNA clone, SEQ ID NO 1223.

XX lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
 KW human; clone; ss.

XX Homo sapiens.

PN WO2003037267-A2.

XX 08-MAY-2003.

XX 28-OCT-2002; 2002WO-US034777.

XX 29-OCT-2001; 2001US-00017754.

XX 28-MAR-2002; 2002US-00113872.

XX (CORI-) CORIXA CORP.

XX Henderson RA, Wang T, Watanabe Y, Kalos MD, Sleath PR;

PI Johnson JC, Retter MW, Durham M, Carter D, Fanger GR, Vedwick TS;

PI Bangur CS, McNabb A;

XX WPI; 2003-468346/44.

XX New polypeptides and encoding polynucleotides, useful for diagnosing,
 PT preventing and/or treating lung cancer.

XX Example 1; SEQ ID NO 1223; 258pp; English.

XX The invention relates to novel compositions and methods for the therapy
 CC and diagnosis of cancer, particularly lung cancer. The compositions
 CC comprise one or more lung tumour polypeptides, immunogenic portions
 CC thereof, polynucleotides that encode such polypeptides, antigen presenting
 CC cells that express such polypeptides, and T cells that are specific for
 CC cells expressing such polypeptides. The novel compositions have
 CC cytostatic and immunostimulant activity. The lung tumour antigens can be

CC used in the creation of a vaccine. The polynucleotides that encode the
CC lung tumour polypeptides can be used in gene therapy to help in the
CC treatment of lung tumours. This polynucleotide sequence represents a
CC human lung tumour cDNA clone of the invention. This sequence was not
CC shown in the specification. It has been taken from a World Intellectual
CC Property Organization CD ROM supplied with the specification.
XX

SQ Sequence 390 BP; 96 A; 92 C; 83 G; 119 T; 0 U; 0 Other;
Query Match 16.8%; Score 31; DB 10; Length 390;
Best Local Similarity 48.8%; Pred. NO. 8.4;
Matches 82; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 14 CTTGATCTATTTCATTTGATCAAGGATTATACACAAACAAGAGACATCCATGCCGG 73
DB 175 CATGAAATCTCTGTTTCGTAGCAAGTGCATGCTCACAGTTGTCAGTCTGCCACTCCGAG 234
QY 74 TTAAGCAGTATCGTTCCATCTAACAAGAGAGGCTGCATGAAAGGAGGTGATGGGTTTT 133
DB 235 TTTATTGGTGTGTTTCTTTGAGATCCATGCTTCTGGTTGAATCTCCTGGAACTC 294
QY 134 TCATCTTAGGATGACAGAACATACGGATGAAAAAGGAGAGGGATG 181
DB 295 CCTCATTAGGTATGAAATAGCATGATGCATTGCATTAAGTCACGAAGG 342

Search completed: November 10, 2004, 17:09:37
Job time : 121.352 secs

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Query Match 99.5%; Score 184; DB 3; Length 185;
 Best Local Similarity 100.0%; Pred. No. 5.7e-52; Indels 0; Gaps 0;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACCGCCTTGATCTATTTTCATTTGATCAAGGATTTATACAAACAAAGAGA 60
 DB 1 TCATGTAACCGCCTTGATCTATTTTCATTTGATCAAGGATTTATACAAACAAAGAGA 60

QY 61 CATCATGCGGGGTTAAAGCAGTATCGTTCATCTAAACAGAGAGGCTGCATGAAAGGA 120
 DB 61 CATCATGCGGGGTTAAAGCAGTATCGTTCATCTAAACAGAGAGGCTGCATGAAAGGA 120

QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACGGATGAAAAAGGAGGGAT 180
 DB 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACGGATGAAAAAGGAGGGAT 180

QY 181 GGAAA 185
 DB 181 GGAAA 185

RESULT 2
 US-08-470-953A-26
 ; Sequence 26, Application US/08470953A
 ; Patent No. 6346407
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDREE LAHAYE
 ; APPLICANT: ERIC DE BUYL
 ; APPLICANT: PIERRE LEDOUX
 ; APPLICANT: RENE DETROZ
 ; TITLE OF INVENTION: Xylanase, microorganisms produced it,
 ; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
 ; TITLE OF INVENTION: and uses thereof
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
 ; STREET: 2000 K St., N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,953A
 ; FILING DATE: 6-OCTOBER-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilhem P. Gadiano, Esq.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-40
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-429-0625
 ; TELEFAX: (202) 293-1850
 ; TELEX: 650 383-5605
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 185 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-470-953A-26

Query Match 99.5%; Score 184; DB 3; Length 185;
 Best Local Similarity 100.0%; Pred. No. 5.7e-52;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACCGCCTTGATCTATTTTCATTTGATCAAGGATTTATACAAACAAAGAGA 60
 DB 1 TCATGTAACCGCCTTGATCTATTTTCATTTGATCAAGGATTTATACAAACAAAGAGA 60

QY 61 CATCATGCGGGGTTAAAGCAGTATCGTTCATCTAAACAGAGAGGCTGCATGAAAGGA 120
 DB 61 CATCATGCGGGGTTAAAGCAGTATCGTTCATCTAAACAGAGAGGCTGCATGAAAGGA 120

QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACGGATGAAAAAGGAGGGAT 180
 DB 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAAACAATACGGATGAAAAAGGAGGGAT 180

QY 181 GGAAA 185
 DB 181 GGAAA 185

RESULT 3
 US-09-076-677-28
 ; Sequence 28, Application US/09076677
 ; Patent No. 6423523
 ; GENERAL INFORMATION:
 ; APPLICANT: DE BUYL, ERIC
 ; LAHAYE, ANDREE
 ; LEDOUX, PIERRE
 ; AMORY, ANTOINE
 ; DETROZ, RENE
 ; ANDRE, CHRISTOPHE
 ; VETTER, ROMAN
 ; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
 ; EXPRESSION VECTORS FOR SUCH XYLANASE AND
 ; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 ; USE THEREOF
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
 ; STREET: 2000 K St., N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/076,677
 ; FILING DATE: 12-May-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/275,526
 ; FILING DATE: 15-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gadiano, Wilhem P.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-49
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 429-0625
 ; TELEFAX: (202) 293-0625
 ; TELEX: 650 383 5605
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 185 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: genomic DNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 ; US-09-076-677-28

Query Match 99.5%; Score 184; DB 4; Length 185;

	Best Local Similarity	100.0%;	Pred. No. 5.7e-52;			
	Matches	185;	Conservative	0;	Mismatches	0;
					Indels	Gaps
Qy	1	TCATGTAACTCGCGCTTGATCTATTTCATTTGTATCAAGGATTTATACACAACCAAGAGA	60			
Db	1	TCATGTAACTCGCGCTTGATCTATTTCATTTGTATCAAGGATTTATACACAACCAAGAGA	60			
Qy	61	CATCCATGCCGGGTTAAAGCAGATATCGTTCATCTAACGAGAAAGNCGTGCATGAAAGGA	120			
Db	61	CATCCATGCCGGGTTAAAGCAGATATCGTTCATCTAACGAGAAAGNCGTGCATGAAAGGA	120			
Qy	121	GGTATCGGGTTTTTCATCTTAGGGATCAGACACATACGGATGAAAAAGCAGAGGGAT	180			
Db	121	GGTATCGGGTTTTTCATCTTAGGGATCAGACACATACGGATGAAAAAGCAGAGGGAT	180			
Qy	181	GGAAA	185			
Db	181	GGAAA	185			

RESULT 4

US-001-073-055-28
Sequence 28, Application US/09073055
Patent No. 6426211
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
LAHAYE, ANDR E
LEDoux, PIERRE
AMORY, ANTOINE
DETROZ, REN
ANDRE, CHRISTOPHE
VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-073-055-28

US-09-073-055-28

	Query Match	Best Local Similarity	99.5%; Matches 185;	Score 184; Conservative 0;	DB 4; Mismatches 0;	Length 185; Indels 0;	Gaps 0;
Qy	1	TCATGTAACTCGGCTTGGATCTATTTCATTTTGTATCAAAGGATTTATACAAACAAGAGA	60				
Dd	1	TCATGTAACTCGGCTTGGATCTATTTCATTTTGTATCAAAGGATTTATACAAACAAGAGA	60				
Qy	61	CATCCATGCGGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAAGGA	120				
Dd	61	CATCCATGCGGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAAGGA	120				
Qy	121	GGTGATGGGTTTTTTTCATCTTAGGGATGACAGAACATACGGATCGAAAAAAGGAGAGGGAT	180				
Dd	121	GGTGATGGGTTTTTTTCATCTTAGGGATGACAGAACATACGGATCGAAAAAAGGAGAGGGAT	180				
Qy	181	GGAAA	185				
Dd	181	GGAAA	185				

RESULT 5

US-08-275-526C-1
 Sequence 1, Application US/08275526C
 Patent No. 6180382
 GENERAL INFORMATION:
 APPLICANT: DE BUYL, ERIC
 APPLICANT: LAHAYE, ANDR E
 APPLICANT: LEDOUX, PIERRE
 APPLICANT: AMORY, ANTOINE
 APPLICANT: DETROZ, REN
 APPLICANT: ANDRE, CHRISTOPHE
 APPLICANT: VETTER, ROMAN
 TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
 TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
 TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
 TITLE OF INVENTION: USE THEREOF
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
 STREET: 2000 K St., N.W., Suite 200
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/275,526C
 FILING DATE: 15-JUL-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gadiano, Wilhem F.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 4121-49
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 429-0625
 TELEFAX: (202) 293-0625
 TELEX: 650 383 5605
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1022 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Bacillus pumilus
 STRAIN: PRL B12

US-08-275-526C-1

Query Match 99.5%; Score 184; DB 3; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATGTAACCTCGCCTTGATCTATTTTCATTTGATCAAGAGGATTTATACACAAACAAGAGA 60
Db 1 TCATGTAACCTCGCCTTGATCTATTTTCATTTGATCAAGAGGATTTATACACAAACAAGAGA 60

Qy 61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAAGGA 120
Db 61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAAGGA 120

Qy 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAAACATACCGATGAAAAAGGAGGGAT 180
Db 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAAACATACCGATGAAAAAGGAGGGAT 180

Qy 181 GGAAA 185
Db 181 GGAAA 185

RESULT 6

US-08-275-526C-35
; Sequence 35, Application US/08275526C
; Patent No. 6180382
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: LAHAYE, ANDR E
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE
; APPLICANT: DETROZ, REN
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; EXPRESSION VECTORS FOR SUCH XYLANASE AND
; TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,526C
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-275-526C-35

Query Match 99.5%; Score 184; DB 3; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATGTAACCTCGCCTTGATCTATTTTCATTTGATCAAGAGGATTTATACACAAACAAGAGA 60
Db 1 TCATGTAACCTCGCCTTGATCTATTTTCATTTGATCAAGAGGATTTATACACAAACAAGAGA 60

Qy 61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAAGGA 120
Db 61 CATCCATCCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAAGGA 120

Qy 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAAACATACCGATGAAAAAGGAGGGAT 180
Db 121 GGTGATGGGTTTTTCATCTTAGGATGACAGAAACATACCGATGAAAAAGGAGGGAT 180

Qy 181 GGAAA 185
Db 181 GGAAA 185

RESULT 7

US-09-076-677-1
; Sequence 1, Application US/09076677
; Patent No. 6423523
; GENERAL INFORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: LAHAYE, ANDREE
; APPLICANT: LEDOUX, PIERRE
; APPLICANT: AMORY, ANTOINE
; APPLICANT: DETROZ, RENE
; APPLICANT: ANDRE, CHRISTOPHE
; APPLICANT: VETTER, ROMAN
; TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
; EXPRESSION VECTORS FOR SUCH XYLANASE AND
; OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
; USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K St., N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,677
; FILING DATE: 12-May-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/275,526
; FILING DATE: 15-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gadiano, Wilhem F.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-0625
; TELEEX: 650 383 5605
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE:

ORGANISM: Bacillus pumilus
STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-076-677-1

Query Match 99.5%; Score 184; DB 4; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACCTCGCCTTGATCTATTTCATTTGTATCAAAAGGATTTATACACAAACAAGAGA 60
DB 1 TCATGTAACCTCGCCTTGATCTATTTCATTTGTATCAAAAGGATTTATACACAAACAAGAGA 60

QY 61 CATCCATGCCGGTTAAAGCAGTATCGTTCCATCTAACAGAGAGAGGCTGCAATGAAGGA 120
DB 61 CATCCATGCCGGTTAAAGCAGTATCGTTCCATCTAACAGAGAGAGGCTGCAATGAAGGA 120

QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAAGGAGGGAT 180
DB 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAAGGAGGGAT 180

QY 181 GGAAA 185
DB 181 GGAAA 185

RESULT 8
US-09-076-677-35
Sequence 35, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
LAHAYE, ANDREE
LEDoux, PIERRE
AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-5605
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-076-677-35

Query Match 99.5%; Score 184; DB 4; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACCTCGCCTTGATCTATTTCATTTGTATCAAAAGGATTTATACACAAACAAGAGA 60
DB 1 TCATGTAACCTCGCCTTGATCTATTTCATTTGTATCAAAAGGATTTATACACAAACAAGAGA 60

QY 61 CATCCATGCCGGTTAAAGCAGTATCGTTCCATCTAACAGAGAGAGGCTGCAATGAAGGA 120
DB 61 CATCCATGCCGGTTAAAGCAGTATCGTTCCATCTAACAGAGAGAGGCTGCAATGAAGGA 120

QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAAGGAGGGAT 180
DB 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAAGGAGGGAT 180

QY 181 GGAAA 185
DB 181 GGAAA 185

RESULT 9
US-09-073-055-1
Sequence 1, Application US/09073055
Patent No. 6426211
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
LAHAYE, ANDR E
LEDoux, PIERRE
AMORY, ANTOINE
DETROZ, REN
ANDRE, CHRISTOPHE
VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-5605
INFORMATION FOR SEQ ID NO: 1:
INFORMATION FOR SEQ ID NO: 1:

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/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 1022 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
/ ORIGINAL SOURCE:
/   ORGANISM: Bacillus pumilus
/   STRAIN: PRL B12
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-073-055-1

Query Match          99.5%; Score 184; DB 4; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACCTCGCTTGATCTATTTCATTTGATCAAGGATTTATACACAAACAAGAGA 60
Db 1 TCATGTAACCTCGCTTGATCTATTTCATTTGATCAAGGATTTATACACAAACAAGAGA 60
QY 61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAGGA 120
Db 61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAGGA 120
QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAAGGAGGGAT 180
Db 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAAGGAGGGAT 180
QY 181 GGAAA 185
Db 181 GGAAA 185

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RESULT 10
US-09-073-055-35
/ Sequence 35, Application US/09073055
/ Patent No. 6426211
/ GENERAL INFORMATION:
/   APPLICANT: DE BUYL, ERIC
/   LAHAYE, ANDR E
/   LEBDOUX, PIERRE
/   AMORY, ANTOINE
/   DETROZ, REN
/   ANDRE, CHRISTOPHE
/   VETTER, ROMAN
/ TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
/   EXPRESSION VECTORS FOR SUCH XYLANASE AND
/   OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
/   USE THEREOF
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/   ADDRESSER: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
/   STREET: 2000 K St., N.W., Suite 200
/   CITY: Washington
/   STATE: D.C.
/   COUNTRY: U.S.A.
/   ZIP: 20006
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/073,055
/   FILING DATE: 05-May-1998
/   CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US/08/275,526
/   FILING DATE: 15-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Gadiano, Wilhelm F.
/   REGISTRATION NUMBER: 37,136
/   REFERENCE/DOCKET NUMBER: 4121-49

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/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (202) 429-0625
/   TELEFAX: (202) 293-0625
/   TELEX: 650 383 5605
/ INFORMATION FOR SEQ ID NO: 35:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 1022 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-073-055-35

Query Match          99.5%; Score 184; DB 4; Length 1022;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACCTCGCTTGATCTATTTCATTTGATCAAGGATTTATACACAAACAAGAGA 60
Db 1 TCATGTAACCTCGCTTGATCTATTTCATTTGATCAAGGATTTATACACAAACAAGAGA 60
QY 61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAGGA 120
Db 61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAGGA 120
QY 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAAGGAGGGAT 180
Db 121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGATGAAAAAAGGAGGGAT 180
QY 181 GGAAA 185
Db 181 GGAAA 185

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RESULT 11
US-08-232-463-14/c
/ Sequence 14, Application US/08232463
/ Patent No. 5670367
/ GENERAL INFORMATION:
/   APPLICANT: DORNER, F.
/   APPLICANT: SCHEIFLINGER, F.
/   APPLICANT: FALKNER, F. G.
/ TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Foley & Lardner
/   STREET: 1800 Diagonal Road, Suite 500
/   CITY: Alexandria
/   STATE: VA
/   COUNTRY: USA
/   ZIP: 22313-0299
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/232,463
/   FILING DATE:
/   CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US/07/935,313
/   FILING DATE:
/   APPLICATION NUMBER: EP 91 114 300.6
/   FILING DATE: 26-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/   NAME: BENT, Stephen A.
/   REGISTRATION NUMBER: 29,768
/   REFERENCE/DOCKET NUMBER: 30472/114 IMMU
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (703)836-9300
/   TELEFAX: (703)683-4109

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; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-Fls
; US-08-232-463-14

Query Match      19.4%; Score 35.8; DB 1; Length 7218;
Best Local Similarity 15.2%; Pred. No. 0.059;
Matches 25; Conservative 78; Mismatches 61; Indels 0; Gaps 0;

QY 22 ATTTCATTTGTATCAAGAGTTTATACACAAACAGAGACATCCATGCGGGTTAAAGCA 81
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QY 82 GTATCGTTCCTAACAAGAGAGGCTGCATGAAGAGGAGTGATGGGTTTTCATCTTA 141
Db 1420 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1361
QY 142 GCGATCAGACAAATACCGGATGAAAGAGGAGGATGCGAAA 185
Db 1360 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1317

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RESULT 12
US-08-956-171E-38
; Sequence 38, Application US/08956171E
; Patent No. 659114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS, version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23439 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-956-171E-38

Query Match      17.4%; Score 32.2; DB 4; Length 23439;
Best Local Similarity 52.2%; Pred. No. 1.5;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 44 TATACACAAACAGAGACATCCATGCCGGTTAAAGCAGTATCGTTCATCTAACAGAGA 103
Db 11481 TATGTATATAACGTGTGATGGACTTAGGCGTTCATTTGTCAGTCGTTGGTGGCGATTAAC 11540
QY 104 AGGCTGTCATGAAGAGGAGTGTATGGTGTTCATCTTAGGGGATGACAGAACAAATACGGAT 163
Db 11541 ACGACCAAAAGAAATTACGAAACGTTTGTTCACAAATTATGGAAGATTAAATGATACCGAT 11600
QY 164 GAAAGAGGAGGAGG 177
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RESULT 13
US-08-781-986A-38
; Sequence 38, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS, version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-38

Query Match      17.4%; Score 32.2; DB 4; Length 23439;
Best Local Similarity 52.2%; Pred. No. 1.5;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Qy 164 GAAAAAAGGAGAGG 177
Db 11601 AAAAAAACGAGATG 11614

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RESULT 14

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US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
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; US-08-916-421B-1

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Query Match 17.0%; Score 31.4; DB 4; Length 1664976;
Best Local Similarity 59.6%; Pred. No. 17;
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QY 77 AGCAGTATCGTTCCATCTAACAGAGAAG 105
Db 492403 ATTCAGATTTTCTTTTCAACTGAGAAG 492431

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RESULT 15
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; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6797466
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

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Query Match 17.0%; Score 31.4; DB 4; Length 1664976;

Best Local Similarity 59.6%; Pred. No. 17;

Matches 53; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 17 GATCTATTTCATTTGTATCAAGGATTATACAAAGACATCCATCGCGGGTTA 76

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Db 492403 ATTCAGATTTTCTTTTCAACTGAGAAG 492431

Search completed: November 11, 2004, 01:34:27
Job time : 25.2524 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2004, 21:26:43 ; Search time 118.282 Seconds
(without alignments)
8421.106 Million cell updates/sec

Title: US-09-909-207-26

Perfect score: 185
Sequence: 1 TCATGTAACCTCCCTTGATC.....AAAAGGAGAGGATGGA 185

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	184	99.5	185	9	US-09-909-207-26
2	37	20.0	634	13	Sequence 26, Appl
3	37	20.0	634	15	Sequence 209848,
4	35	18.9	624	13	Sequence 209848,
5	35	18.9	624	15	Sequence 182736,
6	34.8	18.8	1500	15	Sequence 182736,
7	33.2	17.9	260803	17	Sequence 46834, A
8	33	17.8	445	16	Sequence 84, Appl
9	32.8	17.7	355	16	Sequence 8116, Ap
10	32.8	17.7	3045	15	Sequence 141151,
11	32.2	17.4	23439	8	Sequence 41036, A
12	32.2	17.4	23439	16	Sequence 38, Appl
					Sequence 38, Appl

C 13	32	17.3	405	9	US-09-960-352-4132	Sequence 4132, Ap
C 14	31.6	17.1	1079	13	US-10-027-632-117073	Sequence 117073,
C 15	31.6	17.1	1079	15	US-10-027-632-117073	Sequence 117073,
C 16	31.6	17.1	684973	9	US-09-263-959-1	Sequence 1, Appl
C 17	31.2	16.9	326	18	US-10-425-115-72247	Sequence 72247, A
C 18	31.2	16.9	497	16	US-10-424-599-115848	Sequence 115848,
C 19	31	16.8	390	9	US-09-736-457-1223	Sequence 1223, Ap
C 20	31	16.8	390	9	US-09-902-941-1223	Sequence 1223, Ap
C 21	31	16.8	390	9	US-09-849-626-1223	Sequence 1223, Ap
C 22	31	16.8	390	14	US-10-017-754-1223	Sequence 1223, Ap
C 23	31	16.8	390	15	US-10-113-872-1223	Sequence 1223, Ap
C 24	31	16.8	390	15	US-10-283-017-1223	Sequence 1223, Ap
C 25	31	16.8	32183	9	US-09-764-869-1494	Sequence 1494, Ap
C 26	31	16.8	32183	14	US-10-091-504-1494	Sequence 1494, Ap
C 27	31	16.8	32183	16	US-10-227-577-1494	Sequence 1494, Ap
C 28	31	16.8	301692	16	US-10-428-487-11	Sequence 11, Appl
C 29	31	16.8	310268	17	US-10-367-094-195	Sequence 195, App
C 30	30.8	16.6	804	13	US-10-027-632-128655	Sequence 128655,
C 31	30.8	16.6	804	15	US-10-027-632-128655	Sequence 128655,
C 32	30.8	16.6	1132	9	US-09-938-842A-3452	Sequence 3452, Ap
C 33	30.8	16.6	1132	11	US-09-938-842A-3452	Sequence 496, App
C 34	30.6	16.5	58723	13	US-10-087-192-496	Sequence 16465, A
C 35	30.2	16.3	930	16	US-10-282-122A-16465	Sequence 282580,
C 36	30	16.2	561	13	US-10-027-632-282580	Sequence 282580,
C 37	30	16.2	561	15	US-10-027-632-282580	Sequence 18, Appl
C 38	30	16.2	831	16	US-10-305-720-18	Sequence 264187,
C 39	29.8	16.1	646	13	US-10-027-632-264187	Sequence 264187,
C 40	29.8	16.1	646	15	US-10-027-632-264187	Sequence 53, Appl
C 41	29.8	16.1	178896	17	US-10-450-826-53	Sequence 6389, Ap
C 42	29.6	16.0	422	18	US-10-674-124A-6389	Sequence 478, App
C 43	29.6	16.0	610	14	US-10-116-802-478	Sequence 948, App
C 44	29.6	16.0	977	10	US-09-764-872-948	Sequence 49, Appl
C 45	29.6	16.0	1143	9	US-09-738-626-49	

ALIGNMENTS

RESULT 1

US-09-909-207-26
Sequence 26, Application US/09909207
Patent No. US20020115181A1

GENERAL INFORMATION:

APPLICANT: ANDREE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSER: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: US/09/909,207

APPLICATION NUMBER: 19-Jul-2001

FILING DATE: 19-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/470,953

FILING DATE: 06-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Wilhem F. Gadiano, Esq.

REGISTRATION NUMBER: 37,136

REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-909-207-26

Query Match 99.5%; Score 184; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 6.4e-49;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGTAACGCTGCTGATCTATTTTCATTTCTATCAAGGATTTATACAAACAAGAGA 60
DB 1 TCATGTAACGCTGCTGATCTATTTTCATTTCTATCAAGGATTTATACAAACAAGAGA 60

QY 61 CATCATCGCGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAAGGA 120
DB 61 CATCATCGCGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGCTGCATGAAAGGA 120

QY 121 GGTGATGGTTTTTCATCTTAGGATGACAGAACTACCGATGAAAAAGAGAGGAT 180
DB 121 GGTGATGGTTTTTCATCTTAGGATGACAGAACTACCGATGAAAAAGAGAGGAT 180

QY 181 CGAAA 185
DB 181 CGAAA 185

RESULT 2
US-10-027-632-209848/c
; Sequence 209848, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209848
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-209848

Query Match 20.0%; Score 37; DB 13; Length 634;
Best Local Similarity 52.7%; Pred. No. 0.18;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 36 AAAGGATTTATACAAAACAGACATCCATCGCGGTTAAAGCAGTATCGTTCCATCT 95
DB 250 AAAGGATCAACAATAAACAGATGACCTACAGACAGGTGATATATTAGCAATCAACTT 191

QY 96 AACAGAGAAGGCTGCATGAAAAGGAGGTGATGGGTTTTTCATCTTAGGGATGACAGACA 155
DB 190 ATCTAACAGGAATTAATAACTGGAATATATAAGTAATTCAAACATCTCAATAAAAAATA 131

QY 156 ATACGGATGAAAAAGGAGGATGGA 185
DB 130 ATTTGATTAATAATGGGTAAGAATTGAA 101

RESULT 3
US-10-027-632-209848/c
; Sequence 209848, Application US/10027632
; Publication No. US20020204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209848
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-209848

Query Match 20.0%; Score 37; DB 15; Length 634;
Best Local Similarity 52.7%; Pred. No. 0.18;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 36 AAAGGATTTATACAAAACAGACATCCATCGCGGTTAAAGCAGTATCGTTCCATCT 95
DB 250 AAAGGATCAACAATAAACAGATGACCTACAGACAGGTGATATATTAGCAATCAACTT 191

QY 96 AACAGAGAAGGCTGCATGAAAAGGAGGTGATGGGTTTTTCATCTTAGGGATGACAGACA 155
DB 190 ATCTAACAGGAATTAATAACTGGAATATATAAGTAATTCAAACATCTCAATAAAAAATA 131

QY 156 ATACGGATGAAAAAGGAGGATGGA 185
DB 130 ATTTGATTAATAATGGGTAAGAATTGAA 101

RESULT 4
US-10-027-632-182736/c
; Sequence 182736, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632

```

; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182736
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-182736

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Query Match      18.9%; Score 35; DB 13; Length 624;
Best Local Similarity 51.3%; Pred. No. 0.79;
Matches 80; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 18 ATCTATTTTCATTTGTTATCAAGGATTTATACAAACAGAGACATCCATGCCGGTTAA 77
DB 503 ATCAATATGTTTGAATGAGAAAGAGCTACCAATAAACAGAAACAAATAGACAGGAAG 444
QY 78 AGCAGTATCGTTCATCTTAACAGAGAGGNCCTGATGAAGAGGATGATGGGTTTTCAT 137
DB 443 AGCAGTATCATGAGACTGATGGAAGAAAGCTAAAGGAAAGCTGATGAATAGTATTGAA 384
QY 138 CTTAGGATGACAGAACAAATACGGATGAAAAAGGA 173
DB 383 GTTAGAAATTTACAAAAATAAAAACAATAAAGTGA 348

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RESULT 5
US-10-027-632-182736/c
; Sequence 182736, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182736
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-182736

```

```

Query Match      18.9%; Score 35; DB 15; Length 624;
Best Local Similarity 51.3%; Pred. No. 0.79;
Matches 80; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 18 ATCTATTTTCATTTGTTATCAAGGATTTATACAAACAGAGACATCCATGCCGGTTAA 77
DB 503 ATCAATATGTTTGAATGAGAAAGAGCTACCAATAAACAGAAACAAATAGACAGGAAG 444
QY 78 AGCAGTATCGTTCATCTTAACAGAGAGGNCCTGATGAAGAGGATGATGGGTTTTCAT 137
DB 443 AGCAGTATCATGAGACTGATGGAAGAAAGCTAAAGGAAAGCTGATGAATAGTATTGAA 384
QY 138 CTTAGGATGACAGAACAAATACGGATGAAAAAGGA 173
DB 383 GTTAGAAATTTACAAAAATAAAAACAATAAAGTGA 348

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RESULT 6
US-10-369-493-46834
; Sequence 46834, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46834
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-10-369-493-46834

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Query Match      18.8%; Score 34.8; DB 15; Length 1500;
Best Local Similarity 65.4%; Pred. No. 1.3;
Matches 51; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 20 CTATTTTCATTTGTTATCAAGGATTTATACAAACAGAGACATCCATGCCGGTTAAAG 79
DB 1423 CTATTTGATTTGTTATGAAGAACTTTACACTCACAAAGGATCTCAATACAGCTTTGAAG 1482
QY 80 CAGTATCGTTCATCTAA 97
DB 1483 AGCTTCGAAAAAATAA 1500

```

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RESULT 7
US-10-388-838-84/c
; Sequence 84, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 260803
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

```

; LOCATION: (1)...(260803)
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-388-838-84

Query Match 17.9%; Score 33.2; DB 17; Length 260803;
 Best Local Similarity 48.6%; Pred. No. 35;
 Matches 89; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 2 CATGTAACCTCGCCTTGATCTATTTCATTTCTGATCAAGAGATTTTATACAAAACAAGAGAC 61
 DB 183802 CATGTAATAATGTTTAGAGCTGCTAAAGTTTCTAGCAGTTTCTTATGGCAGCAACAGAAAAAC 183743

QY 62 ATCCATCCCGGTTTAAAGCAGTATCGTTCCATCTAACAGAGAAGNCTGCATGAAGAGG 121
 DB 183742 TACCATAATTTGGGTACAGATTACCATCTTACAACTAAGAAATCAGAAAAATACATTAA 183693

QY 122 GTGATGGTTTTTCATCTTTAGGATGACAGAAACAATACGGATCAAAAAAGGAGGATG 181
 DB 183682 ATTATGGCTTTCTGATCTTGGACAACAGGCGACACAGGAGCAATCACTAAGAGAGCT 183623

QY 182 GAA 184
 DB 183622 GAA 183620

RESULT 8
 US-10-424-599-8116/C
 ; Sequence 8116, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 8116
 ; LENGTH: 445
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_107339C.1
 US-10-424-599-8116

Query Match 17.8%; Score 33; DB 16; Length 445;
 Best Local Similarity 50.8%; Pred. No. 3;
 Matches 78; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 20 CTATTTTCATTGTATCAAAAGGATTTATACAAAACAAGAGACATCCATCGCGGTTAAAG 79
 DB 245 CAAATTCATAATAAAGAAATCAATTAATCTAAATACATTTTCTTTTATTTGCTTAAA 186

QY 80 CAGTATCGTTCCATCTAACAGAGAAGNCTGCATGAAGAGAGTGAATGGGTTTTTCATCT 139
 DB 185 CATTTTCTCTTTTGGAAACTGAAATAGTATGTTTAAATATATGATTTAGTTTTTTTCT 126

QY 140 TAGGGATGACAGAAACAATACGGATGAAAAAGGA 173
 DB 125 TCTTTTCTTAAATATATATATATATATATGA 92

RESULT 9
 US-10-424-599-141151/C
 ; Sequence 141151, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 8116
 ; LENGTH: 445
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_107339C.1
 US-10-424-599-8116

Query Match 17.7%; Score 32.8; DB 15; Length 3045;
 Best Local Similarity 51.0%; Pred. No. 7.7;
 Matches 76; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 27 ATTTGTATCAAAAGGATTTATACAAAACAAGAGACATCCATCGCGGTTAAAGCAGATC 86
 DB 1496 ATATGGAAGTCGATGTATGCAAAACCAAAAGACATTTGAGGACTATTTTAAACGAACGATC 1555

QY 87 GTTCCATCTAACAGAGAAGNCTGCATGAAGAGGATGATGGGTTTTTCATCTTAGGAT 146
 DB 1556 CGAAAAAGCCGTACATTAGCTGTGAATATATATGATGCGATGCGGCACTCTTTAGGTGGGA 1615

QY 147 GACGAACAATACCGATCAAAAAAGGAGA 175
 DB 1616 TGCACAAGTATCTAGTGTGGAACAGAAA 1644

RESULT 11
 US-08-781-986A-38
 ; Sequence 38, Application US/08781986A
 ; Publication No. US20030054436A1

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE: 27-Dec-2002
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 23439 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-38

Query Match 17.4%; Score 32.2; DB 8; Length 23439;
Best Local Similarity 52.2%; Pred. No. 27;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 44 TATACAAACGAGACATCCATCGCGGTTAAAGCAGTATCGTTCCATCTAACAGAGA 103
DB 11481 TATGTATAAACGCTGTGATGGACTTAGCGGTTTCATCTTAGGGATGACAGAACATACGGAT 11540

QY 104 AGCNCCTGATGAAGAGGATGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGAT 163
DB 11541 ACGACCAAAAGAAATTACGAAACGTTTGTTCAAATTATGGAAGATTAAATGATAACGAT 11600

QY 164 GAAAAAGGAGG 177
DB 11601 AAAAAACGAGATG 11614

RESULT 12
US-10-329-624-38
Sequence 38, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland

COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PID1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 23439 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-10-329-624-38

Query Match 17.4%; Score 32.2; DB 16; Length 23439;
Best Local Similarity 52.2%; Pred. No. 27;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 44 TATACAAACGAGACATCCATCGCGGTTAAAGCAGTATCGTTCCATCTAACAGAGA 103
DB 11481 TATGTATAAACGCTGTGATGGACTTAGCGGTTTCATCTTAGGGATGACAGAACATACGGAT 11540

QY 104 AGCNCCTGATGAAGAGGATGATGGGTTTTTCATCTTAGGGATGACAGAACATACGGAT 163
DB 11541 ACGACCAAAAGAAATTACGAAACGTTTGTTCAAATTATGGAAGATTAAATGATAACGAT 11600

QY 164 GAAAAAGGAGG 177
DB 11601 AAAAAACGAGATG 11614

RESULT 13
US-09-960-352-4132/c
Sequence 4132, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
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NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4132
LENGTH: 405
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: unsure
LOCATION: (372)
OTHER INFORMATION: unsure at all n locations

